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tactccaatt atgttgcacg tacactcatt gtacaggcgt ggagactcat 2650

tgtatgtata agaatatttc tgacagtgag tgacccggag tctctggtgt 2700

accctcttac cagtcagctg cctgcgagca gtcatttttt cctaaaggtt 2750

tacaagtatt tagaactttt cagttcaggg caaaatgttc atgaagttat 2800

tcctcttaaa catggttagg aagctgatga cgttattgat tttgtctgga 2850

ttatgtttct ggaataattt taccaaaaca agctatttga gttttgactt 2900

gacaaggcaa aacatgacag tggattctct ttacaaatgg aaaaaaaaaa 2950

tccttatttt gtataaagga cttccctttt gtaaactaa tccttttat 3000

tggtaaaaat tgtaaattaa aatgtgcaac ttg 3033
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<210> 6
<211> 251
<212> PRT
<213> Homo sapiens

<400> 6
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Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala Ile Thr
 1               5                  10                  15

Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys
                20                  25                  30
```

17

```
Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala
              35              40              45

Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe
              50              55              60

Tyr Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn
              65              70              75

Leu Tyr Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala
              80              85              90

Phe Asp Gly Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn
              95             100             105

Trp Ile Cys Ile Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu
             110             115             120

Leu Met Ile Pro Leu Ile Met Ser Val Leu Tyr Val Trp Ala Gln
             125             130             135

Leu Asn Arg Asp Met Ile Val Ser Phe Trp Phe Gly Thr Arg Phe
             140             145             150

Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu Gly Phe Asn Tyr Ile
             155             160             165

Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly Asn Leu Val Gly
             170             175             180

His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met Asp Leu Gly
             185             190             195

Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg Trp Leu
             200             205             210

Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro Ala
             215             220             225

Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Gly Arg His
             230             235             240

Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln
             245             250
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<210> 7
<211> 1373
<212> DNA
<213> Homo sapiens

<400> 7
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 attaactggt tggtagcttc tatcctgggg gctgagcgac tgcgggccag 100

 ctcttcccct actccctctc ggctccttgt ggcccaaagg cctaaccggg 150

 gtccggcggt ctggcctagg gatcttcccc gttgcccctt tggggcggga 200
```

18

```
tggctgcgga agaagaagac gaggtggagt gggtagtgga gagcatcgcg 250

gggttcctgc gaggcccaga ctggtccatc cccatcttgg actttgtgga 300

acagaaatgt gaagttaact gcaaaggagg gcatgtgata actccaggaa 350

gcccagagcc ggtgattttg gtggcctgtg ttccccttgt ttttgatgat 400

gaagaagaaa gcaaattgac ctatacagag attcatcagg aatacaaaga 450

actagttgaa aagctgttag aaggttacct caaagaaatt ggaattaatg 500

aagatcaatt tcaagaagca tgcacttctc ctcttgcaaa gacccataca 550

tcacaggcca ttttgcaacc tgtgttggca gcagaagatt ttactatctt 600

taaagcaatg atggtccaga aaaacattga aatgcagctg caagccattc 650

gaataattca agagagaaat ggtgtattac ctgactgctt aaccgatggc 700

tctgatgtgg tcagtgacct tgaacacgaa gagatgaaaa tcctgaggga 750

agttcttaga aaatcaaaag aggaatatga ccaggaagaa gaaaggaaga 800

ggaaaaaaca gttatcagag gctaaaacag aagagcccac agtgcattcc 850

agtgaagctg caataatgaa taattcccaa ggggatggtg aacattttgc 900

acacccaccc tcagaagtta aaatgcattt tgctaatcag tcaatagaac 950

ctttgggaag aaaagtggaa aggtctgaaa cttcctccct cccacaaaaa 1000

ggcctgaaga ttcctggctt agagcatgcg agcattgaag gaccaatagc 1050

aaacttatca gtacttggaa cagaagaact tcggcaacga gaacactatc 1100

tcaagcagaa gagagataag ttgatgtcca tgagaaagga tatgaggact 1150

aaacagatac aaaatatgga gcagaaagga aaacccactg gggaggtaga 1200

ggaaatgaca gagaaaccag aaatgacagc agaggagaag caaacattac 1250

taaagaggag attgcttgca gagaaactca agaagaagt tattaataag 1300

taataattaa gaacaatta acaaaatgga agttcaaatt gtcttaaaaa 1350

taaattattt agtccttaca ctg 1373
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<210> 8
<211> 367
<212> PRT
<213> Homo sapiens

<400> 8
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Met Ala Ala Glu Glu Glu Asp Glu Val Glu Trp Val Val Glu Ser
 1               5                  10                  15

Ile Ala Gly Phe Leu Arg Gly Pro Asp Trp Ser Ile Pro Ile Leu
```

```
                20                      25                      30
Asp Phe Val Glu Gln Lys Cys Glu Val Asn Cys Lys Gly Gly His
                35                      40                      45

Val Ile Thr Pro Gly Ser Pro Glu Pro Val Ile Leu Val Ala Cys
                50                      55                      60

Val Pro Leu Val Phe Asp Asp Glu Glu Glu Ser Lys Leu Thr Tyr
                65                      70                      75

Thr Glu Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu Leu
                80                      85                      90

Glu Gly Tyr Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln
                95                      100                     105

Glu Ala Cys Thr Ser Pro Leu Ala Lys Thr His Thr Ser Gln Ala
                110                     115                     120

Ile Leu Gln Pro Val Leu Ala Ala Glu Asp Phe Thr Ile Phe Lys
                125                     130                     135

Ala Met Met Val Gln Lys Asn Ile Glu Met Gln Leu Gln Ala Ile
                140                     145                     150

Arg Ile Ile Gln Glu Arg Asn Gly Val Leu Pro Asp Cys Leu Thr
                155                     160                     165

Asp Gly Ser Asp Val Val Ser Asp Leu Glu His Glu Glu Met Lys
                170                     175                     180

Ile Leu Arg Glu Val Leu Arg Lys Ser Lys Glu Glu Tyr Asp Gln
                185                     190                     195

Glu Glu Glu Arg Lys Arg Lys Lys Gln Leu Ser Glu Ala Lys Thr
                200                     205                     210

Glu Glu Pro Thr Val His Ser Ser Glu Ala Ala Ile Met Asn Asn
                215                     220                     225

Ser Gln Gly Asp Gly Glu His Phe Ala His Pro Pro Ser Glu Val
                230                     235                     240

Lys Met His Phe Ala Asn Gln Ser Ile Glu Pro Leu Gly Arg Lys
                245                     250                     255

Val Glu Arg Ser Glu Thr Ser Ser Leu Pro Gln Lys Gly Leu Lys
                260                     265                     270

Ile Pro Gly Leu Glu His Ala Ser Ile Glu Gly Pro Ile Ala Asn
                275                     280                     285

Leu Ser Val Leu Gly Thr Glu Glu Leu Arg Gln Arg Glu His Tyr
                290                     295                     300

Leu Lys Gln Lys Arg Asp Lys Leu Met Ser Met Arg Lys Asp Met
                305                     310                     315
```

20

Arg Thr Lys Gln Ile Gln Asn Met Glu Gln Lys Gly Lys Pro Thr
                    320   325   330

Gly Glu Val Glu Glu Met Thr Glu Lys Pro Glu Met Thr Ala Glu
                    335   340   345

Glu Lys Gln Thr Leu Leu Lys Arg Arg Leu Leu Ala Glu Lys Leu
                    350   355   360

Lys Glu Glu Val Ile Asn Lys
                    365

<210> 9
<211> 418
<212> DNA
<213> Homo sapiens

<400> 9
gggcacagca catgtgaagt ttttgatgat gaagaagaaa gcaaattgac 50

ctatacagag attcatcagg aatacaaaga actagttgaa aagctgttag 100

aaggttacct caaagaaatt ggaattaatg aagatcaatt tcaagaagca 150

tgcacttctc ctcttgcaaa gacccataca tcacaggcca tttttgcaac 200

ctgtgttggc agcagaagat tttactatct ttaaagcaat gatggtccag 250

aaaaacattg aaatgcagct gcaagccatt cgaataattc aagagagaaa 300

tggtgtatta cctgactgct taaccgatgg ctctgatgtg gtcagtgacc 350

ttgaacacga agagatgaaa atcctgaggg aagttcttag aaaatcaaaa 400

gaggaatatg accaggaa 418

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 10
ttgacctata cagagattca tc 22

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctaagaactt ccctcaggat ttt 23

<210> 12
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
 atgaagatca atttcaagaa gcatgcactt ctcctcttgc 40

<210> 13
<211> 2886
<212> DNA
<213> Homo sapiens

<400> 13
 gcgtggtttt tgttctgcaa taggcggctt agagggaggg gctttttcgc 50

 ctatacctac tgtagcttct ccacgtatgg accctaaagg ctactgctgc 100

 tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 150

 cactagaagc tcttctgagg gaggtaatta aaaaacagtg gaatggaaaa 200

 acagtgctgt agtcatcctg taatatgctc cttgtcaaca atgtatacat 250

 tcctgctagg tgccatattc attgctttaa gctcaagtcg catcttacta 300

 gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 350

 tgtgaatgtg tgctcagaac tggtgaagct agttttctgt gtgcttgtgt 400

 cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 450

 tcctggaagg aattctctga tttcatgaag tggtccattc ctgcctttct 500

 ttatttcctg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 550

 cagccatggc tgttatcttc tcaaatttta gcattataac aacagctctt 600

 ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 650

 cctcctgact ttatttttgt ctattgtggc cttgactgcc gggactaaaa 700

 ctttacagca caacttggca ggacgtggat ttcatcacga tgcctttttc 750

 agcccttcca attcctgcct tcttttcaga agtgagtgtc ccagaaaaga 800

 caattgtaca gcaaaggaat ggacttttcc tgaagctaaa tggaacacca 850

 cagccagagt tttcagtcac atccgtcttg gcatgggcca tgttcttatt 900

 atagtccagt gttttatttc ttcaatggct aatatctata atgaaaagat 950

 actgaaggag gggaaccagc tcactgaaag catcttcata cagaacagca 1000

 aactctattt ctttggcatt ctgtttaatg ggctgactct gggccttcag 1050

22

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aggagtaacc gtgatcagat taagaactgt ggattttttt atggccacag 1100

tgcattttca gtagccctta tttttgtaac tgcattccag ggcctttcag 1150

tggctttcat tctgaagttc ctggataaca tgttccatgt cttgatggcc 1200

caggttacca ctgtcattat cacaacagtg tctgtcctgg tctttgactt 1250

caggccctcc ctggaatttt tcttggaagc cccatcagtc cttctctcta 1300

tatttattta taatgccagc aagcctcaag ttccggaata cgcacctagg 1350

caagaaagga tccgagatct aagtggcaat ctttgggagc gttccagtgg 1400

ggatggagaa gaactagaaa gacttaccaa acccaagagt gatgagtcag 1450

atgaagatac tttctaactg gtacccacat agtttgcagc tctcttgaac 1500

cttattttca cattttcagt gtttgtaata tttatctttt cactttgata 1550

aaccagaaat gtttctaaat cctaatattc tttgcatata tctagctact 1600

ccctaaatgg ttccatccaa ggcttagagt acccaaaggc taagaaattc 1650

taaagaactg atacaggagt aacaatatga agaattcatt aatatctcag 1700

tacttgataa atcagaaagt tatatgtgca gattattttc cttggccttc 1750

aagcttccaa aaaacttgta ataatcatgt tagctatagc ttgtatatac 1800

acatagagat caatttgcca aatattcaca atcatgtagt tctagtttac 1850

atgccaaagt cttccctttt taacattata aaagctaggt tgtctcttga 1900

attttgaggc cctagagata gtcattttgc aagtaaagag caacgggacc 1950

ctttctaaaa acgttggttg aaggacctaa atacctggcc ataccataga 2000

tttgggatga tgtagtctgt gctaaatatt ttgctgaaga agcagtttct 2050

cagacacaac atctcagaat tttaattttt agaaattcat gggaaattgg 2100

atttttgtaa taatcttttg atgttttaaa cattggttcc ctagtcacca 2150

tagttaccac ttgtatttta agtcatttaa acaagccacg gtggggcttt 2200

tttctcctca gtttgaggag aaaaatcttg atgtcattac tcctgaatta 2250

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agctgtgact attgtatatc tttccaagag ttgaaatgct ggcttcagaa 2350

tcataccaga ttgtcagtga agctgatgcc taggaacttt taaagggatc 2400

ctttcaaaag gatcacttag caaacacatg ttgacttttta actgatgtat 2450

gaatattaat actctaaaaa tagaaagacc agtaatatat aagtcacttt 2500
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23

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acagtgctac ttcacactta aaagtgcatg gtatttttca tggtattttg 2550

catgcagcca gttaactctc gtagatagag aagtcaggtg atagatgata 2600

ttaaaaatta gcaaacaaaa gtgacttgct cagggtcatg cagctgggtg 2650

atgatagaag agtgggcttt aactggcagg cctgtatgtt tacagactac 2700

catactgtaa atatgagctt tatggtgtca ttctcagaaa cttatacatt 2750

tctgctctcc tttctcctaa gtttcatgca gatgaatata aggtaatata 2800

ctattatata attcatttgt gatatccaca ataatatgac tggcaagaat 2850

tggtggaaat ttgtaattaa aataattatt aaacct 2886
```

<210> 14
<211> 424
<212> PRT
<213> Homo sapiens

<400> 14

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Met Glu Lys Gln Cys Cys Ser His Pro Val Ile Cys Ser Leu Ser
 1               5                  10                  15

Thr Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser
            20                  25                  30

Ser Ser Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn
            35                  40                  45

Lys Tyr Asp Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu
            50                  55                  60

Val Lys Leu Val Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys
            65                  70                  75

Lys Asp His Gln Ser Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu
            80                  85                  90

Phe Ser Asp Phe Met Lys Trp Ser Ile Pro Ala Phe Leu Tyr Phe
            95                  100                 105

Leu Asp Asn Leu Ile Val Phe Tyr Val Leu Ser Tyr Leu Gln Pro
            110                 115                 120

Ala Met Ala Val Ile Phe Ser Asn Phe Ser Ile Ile Thr Thr Ala
            125                 130                 135

Leu Leu Phe Arg Ile Val Leu Lys Arg Arg Leu Asn Trp Ile Gln
            140                 145                 150

Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser Ile Val Ala Leu Thr
            155                 160                 165

Ala Gly Thr Lys Thr Leu Gln His Asn Leu Ala Gly Arg Gly Phe
            170                 175                 180
```

His His Asp Ala Phe Phe Ser Pro Ser Asn Ser Cys Leu Leu Phe
                185   190   195

Arg Ser Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys Glu Trp
                200   205   210

Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe Ser
                215   220   225

His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys
                230   235   240

Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys
                245   250   255

Glu Gly Asn Gln Leu Thr Glu Ser Ile Phe Ile Gln Asn Ser Lys
                260   265   270

Leu Tyr Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu
                275   280   285

Gln Arg Ser Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr
                290   295   300

Gly His Ser Ala Phe Ser Val Ala Leu Ile Phe Val Thr Ala Phe
                305   310   315

Gln Gly Leu Ser Val Ala Phe Ile Leu Lys Phe Leu Asp Asn Met
                320   325   330

Phe His Val Leu Met Ala Gln Val Thr Thr Val Ile Ile Thr Thr
                335   340   345

Val Ser Val Leu Val Phe Asp Phe Arg Pro Ser Leu Glu Phe Phe
                350   355   360

Leu Glu Ala Pro Ser Val Leu Leu Ser Ile Phe Ile Tyr Asn Ala
                365   370   375

Ser Lys Pro Gln Val Pro Glu Tyr Ala Pro Arg Gln Glu Arg Ile
                380   385   390

Arg Asp Leu Ser Gly Asn Leu Trp Glu Arg Ser Ser Gly Asp Gly
                395   400   405

Glu Glu Leu Glu Arg Leu Thr Lys Pro Lys Ser Asp Glu Ser Asp
                410   415   420

Glu Asp Thr Phe

<210> 15
<211> 755
<212> DNA
<213> Homo sapiens

<400> 15
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25

tcgtggtttt tgttctgcaa taggcggctt agagggaggg gctttttcgc 100

ctatacctac tgtagcttct ccacgtatgg accctaaagg ctactgctgc 150

tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 200

cactagaagc tcttctgagg gaggtaatta aaaaacagtg gaatggaaaa 250

acagtgctgt agtcatcctg taatatgctc cttgtcaaca atgtatacat 300

tcctgctagg tgccatattc attgctttaa gctcaagtcg catcttacta 350

gtgaagtatt ctgccaatga agaaacaag tatgattatc ttccaactac 400

tgtgaatgtg tgctcagaac tggtgaagct agttttctgt gtgcttgtgt 450

cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 500

tcctggaagg aattctctga tttcatgaag tggtccattc ctgcctttct 550

ttatttcctg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 600

cagccatggc tgttatcttc tcaaatttta gcattataac aacagctctt 650

ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 700

cctcctgact ttatttttgt ctattgtggc cttgactgcc gggactaaaa 750

ctttta 755

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
 ctatacctac tgtagcttct 20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
 tcagagaatt ccttccagga 20

<210> 18
<211> 40
<212> DNA
<213> Artificial Sequence

<220>

26

<223> Synthetic oligonucleotide probe

<400> 18
 acagtgctgt agtcatcctg taatatgctc cttgtcaaca 40

<210> 19
<211> 2142
<212> DNA
<213> Homo sapiens

<400> 19
 cggacgcgtg ggcggacgcg tgggcggacg cgtggggccg gcttggctag 50

 cgcgcggcgg ccgtggctaa ggctgctacg aagcgagctt gggaggagca 100

 gcggcctgcg gggcagagga gcatcccgtc taccaggtcc caagcggcgt 150

 ggcccgcggg tcatggccaa aggagaaggc gccgagagcg gctccgcggc 200

 ggggctgcta cccaccagca tcctccaaag cactgaacgc ccggcccagg 250

 tgaagaaaga accgaaaaag aagaaacaac agttgtctgt ttgcaacaag 300

 ctttgctatg cacttggggg agccccctac caggtgacgg gctgtgccct 350

 gggtttcttc cttcagatct acctattgga tgtggctcag gtgggccctt 400

 tctctgcctc catcatcctg tttgtgggcc gagcctggga tgccatcaca 450

 gaccccctgg tgggcctctg catcagcaaa tccccctgga cctgcctggg 500

 tcgccttatg ccctggatca tcttctccac gcccctggcc gtcattgcct 550

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 tccaggactt caatagctct acagtagctt cacaaagtgc caaccataca 850

 catggcacca cttcacacag ggaaacgcaa aaggcatacc tgctggcagc 900

 gggggtcatt gtctgtatct atataatctg tgctgtcatc ctgatcctgg 950

 gcgtgcggga gcagagagaa ccctatgaag cccagcagtc tgagccaatc 1000

 gcctacttcc ggggcctacg gctggtcatg agccacggcc catacatcaa 1050

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 cagaatctac tcctggccat catgctctcg gccactttaa ccattcccat 1200

27

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ctggcagtgg ttcttgaccc ggtttggcaa gaagacagct gtatatgttg 1250

ggatctcatc agcagtgcca tttctcatct tggtggccct catggagagt 1300

aacctcatca ttacatatgc ggtagctgtg gcagctggca tcagtgtggc 1350

agctgccttc ttactaccct ggtccatgct gcctgatgtc attgacgact 1400

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cggaacgtgt caagtttaca ctgaacatgc tcgtgaccat ggctcccata 1600

gttctcatcc tgctgggcct gctgctcttc aaaatgtacc ccattgatga 1650

ggagaggcgg cggcagaata agaaggccct gcaggcactg agggacgagg 1700

ccagcagctc tggctgctca gaaacagact ccacagagct ggctagcatc 1750

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gggatcagga cctgtctgcc ggcttgctga gcagctggac tgcaggtgct 1850

aggaagggaa ctgaagactc aaggaggtgg cccaggacac ttgctgtgct 1900

cactgtgggg ccggctgctc tgtggcctcc tgcctcccct ctgcctgcct 1950

gtggggccaa gccctggggc tgccactgtg aatatgccaa ggactgatcg 2000

ggcctagccc ggaacactaa tgtagaaacc tttttttttac agagcctaat 2050

taataactta atgactgtgt acatagcaat gtgtgtgtat gtatatgtct 2100

gtgagctatt aatgttatta attttcataa aagctggaaa gc 2142
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<210> 20
<211> 458
<212> PRT
<213> Homo sapiens

<400> 20
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Met Trp Leu Arg Trp Ala Leu Ser Leu Pro Pro Ser Ser Cys Leu
 1               5                  10                  15

Trp Ala Glu Pro Gly Met Pro Ser Gln Thr Pro Trp Trp Ala Ser
                20                  25                  30

Ala Ser Ala Asn Pro Pro Gly Pro Ala Trp Val Ala Leu Cys Pro
                35                  40                  45

Gly Ser Ser Ser Pro Arg Pro Trp Pro Ser Leu Pro Thr Ser Ser
                50                  55                  60

Ser Gly Ser Cys Pro Thr Ser His Thr Ala Arg Pro Ile Gly Thr
                65                  70                  75
```

28

Cys Phe Ser Ile Ala Ser Leu Lys Gln Trp Ser Arg Val Ser Met
                80   85   90

Phe Pro Thr Arg Leu Ser Pro Cys Ser Ser Ala Thr Glu Gln Thr
                95   100   105

Glu Arg Asp Ser Ala Thr Ala Tyr Arg Met Thr Val Glu Val Leu
               110   115   120

Gly Thr Val Leu Gly Thr Ala Ile Gln Gly Gln Ile Val Gly Gln
               125   130   135

Ala Asp Thr Pro Cys Phe Gln Asp Phe Asn Ser Ser Thr Val Ala
               140   145   150

Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg Glu
               155   160   165

Thr Gln Lys Ala Tyr Leu Leu Ala Ala Gly Val Ile Val Cys Ile
               170   175   180

Tyr Ile Ile Cys Ala Val Ile Leu Ile Leu Gly Val Arg Glu Gln
               185   190   195

Arg Glu Pro Tyr Glu Ala Gln Gln Ser Glu Pro Ile Ala Tyr Phe
               200   205   210

Arg Gly Leu Arg Leu Val Met Ser His Gly Pro Tyr Ile Lys Leu
               215   220   225

Ile Thr Gly Phe Leu Phe Thr Ser Leu Ala Phe Met Leu Val Glu
               230   235   240

Gly Asn Phe Val Leu Phe Cys Thr Tyr Thr Leu Gly Phe Arg Asn
               245   250   255

Glu Phe Gln Asn Leu Leu Leu Ala Ile Met Leu Ser Ala Thr Leu
               260   265   270

Thr Ile Pro Ile Trp Gln Trp Phe Leu Thr Arg Phe Gly Lys Lys
               275   280   285

Thr Ala Val Tyr Val Gly Ile Ser Ser Ala Val Pro Phe Leu Ile
               290   295   300

Leu Val Ala Leu Met Glu Ser Asn Leu Ile Ile Thr Tyr Ala Val
               305   310   315

Ala Val Ala Ala Gly Ile Ser Val Ala Ala Ala Phe Leu Leu Pro
               320   325   330

Trp Ser Met Leu Pro Asp Val Ile Asp Asp Phe His Leu Lys Gln
               335   340   345

Pro His Phe His Gly Thr Glu Pro Ile Phe Phe Ser Phe Tyr Val
               350   355   360

Phe Phe Thr Lys Phe Ala Ser Gly Val Ser Leu Gly Ile Ser Thr

29

<pre>
                   365   370   375
    Leu Ser Leu Asp Phe Ala Gly Tyr Gln Thr Arg Gly Cys Ser Gln
                    380   385   390

    Pro Glu Arg Val Lys Phe Thr Leu Asn Met Leu Val Thr Met Ala
                    395   400   405

    Pro Ile Val Leu Ile Leu Leu Gly Leu Leu Leu Phe Lys Met Tyr
                    410   415   420

    Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln
                    425   430   435

    Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp
                    440   445   450

    Ser Thr Glu Leu Ala Ser Ile Leu
                    455
</pre>

<210> 21
<211> 571
<212> DNA
<213> Homo sapiens

<400> 21
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 tatataatct gtgctgtcat cctgatcctg ggcgtgcggg agcagagaga 100

 accctatgaa gcccagcagt ctgagccaat cgcctacttc cggggcctac 150

 ggctggtcat gagccacggc ccatacatca aacttattac tggcttcctc 200

 ttcacctcct tggctttcat gctggtggag gggaactttg tcttgttttg 250

 cacctacacc ttgggcttcc gcaatgaatt ccagaatcta ctcctggcca 300

 tcatgctctc ggccacttta accattccca tctggcagtg gttcttgacc 350

 cggtttggca agaagacagc tgtatatgtt gggatctcat cagcagtgcc 400

 atttctcatc ttggtggccc tcatggagag taacctcatc attacatatg 450

 cggtagctgt ggcagctggc atcagtgtgg cagctgcctt cttactaccc 500

 tggtccatgc tgcctgatgt cattgacgac ttccatctga agcagcccca 550

 cttccatgga accgagccca t 571
</pre>

<210> 22
<211> 1173
<212> DNA
<213> Homo sapiens

<400> 22
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30

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aaaggtgcag gtatgagcag gtctgaagac taacattttg tgaagttgta 100

aaacagaaaa cctgttagaa atgtggtggt ttcagcaagg cctcagtttc 150

cttccttcag cccttgtaat ttggacatct gctgctttca tattttcata 200

cattactgca gtaacactcc accatataga cccggcttta ccttatatca 250

gtgacactgg tacagtagct ccagaaaaat gcttatttgg ggcaatgcta 300

aatattgcgg cagttttatg cattgctacc atttatgttc gttataagca 350

agttcatgct ctgagtcctg aagagaacgt tatcatcaaa ttaaacaagg 400

ctggccttgt acttggaata ctgagttgtt taggactttc tattgtggca 450

aacttccaga aaacaaccct ttttgctgca catgtaagtg gagctgtgct 500

tacctttggt atgggctcat tatatatgtt tgttcagacc atcctttcct 550

accaaatgca gcccaaaatc catggcaaac aagtcttctg gatcagactg 600

ttgttggtta tctggtgtgg agtaagtgca cttagcatgc tgacttgctc 650

atcagttttg cacagtggca attttgggac tgatttagaa cagaaactcc 700

attggaaccc cgaggacaaa ggttatgtgc ttcacatgat cactactgca 750

gcagaatggt ctatgtcatt ttccttcttt ggttttttcc tgacttacat 800

tcgtgatttt cagaaaattt ctttacgggt ggaagccaat ttacatggat 850

taaccctcta tgacactgca ccttgcccta ttaacaatga acgaacacgg 900

ctactttcca gagatatttg atgaaaggat aaaatatttc tgtaatgatt 950

atgattctca gggattgggg aaaggttcac agaagttgct tattcttctc 1000

tgaaattttc aaccacttaa tcaaggctga cagtaacact gatgaatgct 1050

gataatcagg aaacatgaaa gaagccattt gatagattat tctaaaggat 1100

atcatcaaga agactattaa aaacacctat gcctatactt ttttatctca 1150

gaaaataaag tcaaaagact atg 1173
```

<210> 23
<211> 266
<212> PRT
<213> Homo sapiens

<400> 23
```
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu
 1               5                  10                  15

Val Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala
                20                  25                  30
```

31

Val Thr Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp
                  35   40   45

Thr Gly Thr Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu
                  50   55   60

Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr
                  65   70   75

Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile Lys
                  80   85   90

Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly
                  95   100   105

Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala
                 110   115   120

His Val Ser Gly Ala Val Leu Thr Phe Gly Met Gly Ser Leu Tyr
                 125   130   135

Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln Pro Lys Ile
                 140   145   150

His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Leu Val Ile Trp
                 155   160   165

Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val Leu
                 170   175   180

His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp
                 185   190   195

Asn Pro Glu Asp Lys Gly Tyr Val Leu His Met Ile Thr Thr Ala
                 200   205   210

Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr
                 215   220   225

Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
                 230   235   240

Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn
                 245   250   255

Asn Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile
                 260   265

<210> 24
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 14, 484
<223> unknown base

<400> 24
cggacgcttg ggcngcgcca gcggccagcg ctagtcggtc tggtaagtgc 50

ctgatgccga gttccgtctc tcgggtcttt tcctggtccc aggcaaagcg 100

gagcggagat cctcaaacgg cctagtgctt cgcgcttccg gagaaaatca 150

gcggtctaat taattcctct ggtttgttga agcagttacc aagaatcttc 200

aacccctttcc cacaaaagct aattgagtac acgttcctgt tgagtacacg 250

ttcctgttga tttacaaaag gtgcaggtat gagcaggtct gaagactaac 300

attttgtgaa gttgtaaaac agaaaacctg ttagaaatgt ggtggtttca 350

gcaaggcctc agtttccttc cttcagccct tgtaatttgg acatctgctg 400

ctttcatatt ttcatacatt actgcagtaa cactccacca tatagacccg 450

gctttacctt atatcagtga cactggtaca gtanc 485

<210> 25
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
acctgttaga aatgtggtgg tttcagcaag gcctcagttt 40

<210> 26
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
ggagatagct gctatgggtt cttcaggcac aacttaacat gggaag 46

<210> 27
<211> 1399
<212> DNA
<213> Homo sapiens

<400> 27
cccacgcgtc cgcccgccgc tgcgtcccgg agtgcaagtg agcttctcgg 50

ctgccccgcg ggccggggtg cggagccgac atgcgcccgc ttctcggcct 100

ccttctggtc ttcgccggct gcaccttcgc cttgtacttg ctgtcgacgc 150

gactgccccg cgggcggaga ctgggctcca ccgaggaggc tggaggcagg 200

tcgctgtggt tcccctccga cctggcagag ctgcgggagc tctctgaggt 250

33

```
ccttcgagag taccggaagg agcaccaggc ctacgtgttc ctgctcttct  300

gcggcgccta cctctacaaa cagggctttg ccatccccgg ctccagcttc  350

ctgaatgttt tagctggtgc cttgtttggg ccatggctgg ggcttctgct  400

gtgctgtgtg ttgacctcgg tgggtgccac atgctgctac ctgctctcca  450

gtatttttgg caaacagttg gtggtgtcct actttcctga taaagtggcc  500

ctgctgcaga gaaaggtgga ggagaacaga aacagcttgt ttttttttctt  550

attgtttttg agactttttcc ccatgacacc aaactggttc ttgaacctct  600

cggccccaat tctgaacatt cccatcgtgc agttcttctt ctcagttctt  650

atcggtttga tcccatataa tttcatctgt gtgcagacag ggtccatcct  700

gtcaacccta acctctctgg atgctctttt ctcctgggac actgtcttta  750

agctgttggc cattgccatg gtggcattaa ttcctggaac cctcattaaa  800

aaatttagtc agaaacatct gcaattgaat gaaacaagta ctgctaatca  850

tatacacagt agaaaagaca catgatctgg attttctgtt tgccacatcc  900

ctggactcag ttgcttattt gtgtaatgga tgtggtcctc taaagcccct  950

cattgttttt gattgccttc tataggtgat gtggacactg tgcatcaatg  1000

tgcagtgtct tttcagaaag gacactctgc tcttgaaggt gtattacatc  1050

aggttttcaa accagccctg gtgtagcaga cactgcaaca gatgcctcct  1100

agaaaatgct gtttgtggcc gggcgcggtg gctcacgcct gtaatcccag  1150

cactttggga ggccgaggcc ggtgattcac aaggtcagga gttcaagacc  1200

agcctggcca agatggtgaa atcctgtctc taataaaaat acaaaaatta  1250

gccaggcgtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag  1300

gcaggagaat tgcttgaacc aaggtggcag aggttgcagt aagccaagat  1350

cacaccactg cactccagcc tgggtgatag agtgagacac tgtcttgac   1399
```

<210> 28
<211> 264
<212> PRT
<213> Homo sapiens

<400> 28

```
Met Arg Pro Leu Leu Gly Leu Leu Leu Val Phe Ala Gly Cys Thr
  1               5                  10                  15

Phe Ala Leu Tyr Leu Leu Ser Thr Arg Leu Pro Arg Gly Arg Arg
                 20                  25                  30
```

34

```
Leu Gly Ser Thr Glu Glu Ala Gly Gly Arg Ser Leu Trp Phe Pro
            35                  40                      45

Ser Asp Leu Ala Glu Leu Arg Glu Leu Ser Glu Val Leu Arg Glu
                50                  55                      60

Tyr Arg Lys Glu His Gln Ala Tyr Val Phe Leu Leu Phe Cys Gly
            65                  70                      75

Ala Tyr Leu Tyr Lys Gln Gly Phe Ala Ile Pro Gly Ser Ser Phe
                80                  85                      90

Leu Asn Val Leu Ala Gly Ala Leu Phe Gly Pro Trp Leu Gly Leu
                95                  100                     105

Leu Leu Cys Cys Val Leu Thr Ser Val Gly Ala Thr Cys Cys Tyr
                110                 115                     120

Leu Leu Ser Ser Ile Phe Gly Lys Gln Leu Val Val Ser Tyr Phe
                125                 130                     135

Pro Asp Lys Val Ala Leu Leu Gln Arg Lys Val Glu Glu Asn Arg
                140                 145                     150

Asn Ser Leu Phe Phe Phe Leu Leu Phe Leu Arg Leu Phe Pro Met
                155                 160                     165

Thr Pro Asn Trp Phe Leu Asn Leu Ser Ala Pro Ile Leu Asn Ile
                170                 175                     180

Pro Ile Val Gln Phe Phe Phe Ser Val Leu Ile Gly Leu Ile Pro
                185                 190                     195

Tyr Asn Phe Ile Cys Val Gln Thr Gly Ser Ile Leu Ser Thr Leu
                200                 205                     210

Thr Ser Leu Asp Ala Leu Phe Ser Trp Asp Thr Val Phe Lys Leu
                215                 220                     225

Leu Ala Ile Ala Met Val Ala Leu Ile Pro Gly Thr Leu Ile Lys
                230                 235                     240

Lys Phe Ser Gln Lys His Leu Gln Leu Asn Glu Thr Ser Thr Ala
                245                 250                     255

Asn His Ile His Ser Arg Lys Asp Thr
                260

<210> 29
<211> 1292
<212> DNA
<213> Homo sapiens

<400> 29
ccgaggcggg aggagcccga gggggcgcga gccccgcatg aatcattgta 50

gtcaatcatt ttccagttct cagccgctca gttgtgatca agggacacgt 100
```

35

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ggtttccgaa ctgccagctc agaataggaa aataacttgg gattttatat 150

tggaagacat ggatcttgct gccaacgaga tcagcattta tgacaaactt 200

tcagagactg ttgatttggt gagacagacc ggccatcagt gtggcatgtc 250

agagaaggca attgaaaaat ttatcagaca gctgctggaa aagaatgaac 300

ctcagagacc ccccccgcag tatcctctcc ttatagttgt gtataaggtt 350

ctcgcaacct tgggattaat cttgctcact gcctactttg tgattcaacc 400

tttcagccca ttagcacctg agccagtgct ttctggagct cacacctggc 450

gctcactcat ccatcacatt aggctgatgt ccttgcccat gccaagaag 500

tacatgtcag aaaataaggg agttcctctg catgggggtg atgaagacag 550

accctttcca gactttgacc cctggtggac aaacgactgt gagcagaatg 600

agtcagagcc cattcctgcc aactgcactg gctgtgccca gaaacacctg 650

aaggtgatgc tcctggaaga cgccccaagg aaatttgaga ggctccatcc 700

actggtgatc aagacgggaa agcccctgtt ggaggaagag attcagcatt 750

ttttgtgcca gtaccctgag gcgacagaag gcttctctga ggggttttc 800

gccaagtggt ggcgctgctt tcctgagcgg tggttcccat ttccttatcc 850

atggaggaga cctctgaaca gatcacaaat gttacgtgag ctttttcctg 900

ttttcactca cctgccattt ccaaaagatg cctctttaaa caagtgctcc 950

tttcttcacc cagaacctgt tgtggggagt aagatgcata agatgcctga 1000

cctatttatc attggcagcg gtgaggccat gttgcagctc atccctccct 1050

tccagtgccg aagacattgt cagtctgtgg ccatgccaat agagccaggg 1100

gatatcggct atgtcgacac cacccactgg aaggtctacg ttatagccag 1150

aggggtccag cctttggtca tctgcgatgg aaccgctttc tcagaactgt 1200

aggaaataga actgtgcaca ggaacagctt ccagagccga aaaccaggtt 1250

gaaaggggaa aaataaaaac aaaaacgatg aaactgcaaa aa 1292
```

<210> 30
<211> 347
<212> PRT
<213> Homo sapiens

<400> 30
```
Met Asp Leu Ala Ala Asn Glu Ile Ser Ile Tyr Asp Lys Leu Ser
1               5                   10                  15

Gln Thr Val Asp Leu Val Arg Gln Thr Gly His Gln Cys Gly Met
```

36

Ser Glu Lys Ala Ile Glu Lys Phe Ile Arg Gln Leu Leu Glu Lys
                    35   40   45

Asn Glu Pro Gln Arg Pro Pro Pro Gln Tyr Pro Leu Leu Ile Val
                    50   55   60

Val Tyr Lys Val Leu Ala Thr Leu Gly Leu Ile Leu Leu Thr Ala
                    65   70   75

Tyr Phe Val Ile Gln Pro Phe Ser Pro Leu Ala Pro Glu Pro Val
                    80   85   90

Leu Ser Gly Ala His Thr Trp Arg Ser Leu Ile His His Ile Arg
                    95   100   105

Leu Met Ser Leu Pro Ile Ala Lys Lys Tyr Met Ser Glu Asn Lys
                   110   115   120

Gly Val Pro Leu His Gly Gly Asp Glu Asp Arg Pro Phe Pro Asp
                   125   130   135

Phe Asp Pro Trp Trp Thr Asn Asp Cys Glu Gln Asn Glu Ser Glu
                   140   145   150

Pro Ile Pro Ala Asn Cys Thr Gly Cys Ala Gln Lys His Leu Lys
                   155   160   165

Val Met Leu Leu Glu Asp Ala Pro Arg Lys Phe Glu Arg Leu His
                   170   175   180

Pro Leu Val Ile Lys Thr Gly Lys Pro Leu Leu Glu Glu Glu Ile
                   185   190   195

Gln His Phe Leu Cys Gln Tyr Pro Glu Ala Thr Glu Gly Phe Ser
                   200   205   210

Glu Gly Phe Phe Ala Lys Trp Trp Arg Cys Phe Pro Glu Arg Trp
                   215   220   225

Phe Pro Phe Pro Tyr Pro Trp Arg Arg Pro Leu Asn Arg Ser Gln
                   230   235   240

Met Leu Arg Glu Leu Phe Pro Val Phe Thr His Leu Pro Phe Pro
                   245   250   255

Lys Asp Ala Ser Leu Asn Lys Cys Ser Phe Leu His Pro Glu Pro
                   260   265   270

Val Val Gly Ser Lys Met His Lys Met Pro Asp Leu Phe Ile Ile
                   275   280   285

Gly Ser Gly Glu Ala Met Leu Gln Leu Ile Pro Pro Phe Gln Cys
                   290   295   300

Arg Arg His Cys Gln Ser Val Ala Met Pro Ile Glu Pro Gly Asp
                   305   310   315

```
Ile Gly Tyr Val Asp Thr Thr His Trp Lys Val Tyr Val Ile Ala
            320             325             330

Arg Gly Val Gln Pro Leu Val Ile Cys Asp Gly Thr Ala Phe Ser
            335             340             345

Glu Leu
```

<210> 31
<211> 478
<212> DNA
<213> Homo sapiens

<400> 31
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ccacggtgtc cgttcttcgc ccggcggcag ctgtccccga ggcgggagga 50

gcccgagggg cgcgagcccc gcatgaatca ttgtagtcaa tcattttcca 100

gttctcagcc gttcagttgt gatcaaggga cacgtggttt ccgaactgcc 150

agctcagaat aggaaaataa cttgggattt tatattggaa gacatggatc 200

ttgctgccaa cgagatcagc atttatgaca actttcaga gactgttgat 250

ttggtgagac agaccggcca tcagtgtggc atgtcagaga aggcaattga 300

aaaatttatc agacagctgc tggaaaagaa tgaacctcag agaccccccc 350

cgcagtatcc tctccttata gttgtgtata aggttctcgc aaccttggga 400

ttaatcttgc tcactgccta ctttgtgatt caacctttca gcccattagc 450

acctgagcca gtgctttgtg gagctcac 478
```
<210> 32
<211> 3531
<212> DNA
<213> Homo sapiens

<400> 32
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ccactgatga ggcagggtcc ccacttgcag ctgcagcagc tgcagcagct 100

gcagagcgct gctcctggct ggtgccactg gtgcgcacgc tgctagaccg 150

tgcctatgag ccgctggggc tgcagtgggg actgccctcc ctgccaccca 200

ccaatggcag ccccaccttc tttgaagact ccaggctttt tgtgccaca 250

cccgaatggc gccacttcat cgacaaacag gtacagccaa ccatgtccca 300

gttcgaaatg gacacgtatg ctaagagcca cgaccttatg tcaggtttct 350

ggaatgcctg ctatgacatg cttatgagca gtgggcagcg gcgccagtgg 400

gagcgcgccc agagtcgtcg ggccttccag gagctggtgc tggaacctgc 450
```

38

```
gcagaggcgg gcgcgcctgg aggggctacg ctacacggca gtgctgaagc 500

agcaggcaac gcagcactcc atggccctgc tgcactgggg ggcgctgtgg 550

cgccagctcg ccagcccatg tggggcctgg gcgctgaggg acactcccat 600

cccccgctgg aaactgtcca gcgccgagac atattcacgc atgcgtctga 650

agctggtgcc caaccatcac ttcgaccctc acctggaagc cagcgctctc 700

cgagacaatc tgggtgaggt tcccctgaca cccaccgagg aggcctcact 750

gcctctggca gtgaccaaag aggccaaagt gagcacccca cccgagttgc 800

tgcaggagga ccagctcggc gaggacgagc tggctgagct ggagaccccg 850

atggaggcag cagaactgga tgagcagcgt gagaagctgg tgctgtcggc 900

cgagtgccag ctggtgacgg tagtggccgt ggtcccaggg ctgctggagg 950

tcaccacaca gaatgtatac ttctacgatg gcagcactga gcgcgtggaa 1000

accgaggagg gcatcggcta tgatttccgg cgcccactgg cccagctgcg 1050

tgaggtccac ctgcggcgtt tcaacctgcg ccgttcagca cttgagctct 1100

tctttatcga tcaggccaac tacttcctca acttcccatg caaggtgggc 1150

acgaccccag tctcatctcc tagccagact ccgagacccc agcctggccc 1200

catcccaccc catacccagg tacggaacca ggtgtactcg tggctcctgc 1250

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atgctgcgtg cctcaggcct tacccagaaa tgggtacagc gtgagatatc 1350

caacttcgag tacttgatgc aactcaacac cattgcgggg cggacctaca 1400

atgacctgtc tcagtaccct gtgttcccct gggtcctgca ggactacgtg 1450

tccccaaccc tggacctcag caacccagcc gtcttccggg acctgtctaa 1500

gcccatcggt gtggtgaacc ccaagcatgc ccagctcgtg agggagaagt 1550

atgaaagctt tgaggaccca gcagggacca ttgacaagtt ccactatggc 1600

acccactact ccaatgcagc aggcgtgatg cactacctca tccgcgtgga 1650

gcccttcacc tccctgcacg tccagctgca aagtggccgc tttgactgct 1700

ccgaccggca gttccactcg gtggcggcag cctggcaggc acgcctggag 1750

agccctgccg atgtgaagga gctcatcccg gaattcttct actttcctga 1800

cttcctggag aaccagaacg gttttgacct gggctgtctc cagctgacca 1850

acgagaaggt aggcgatgtg gtgctacccc cgtgggccag ctctcctgag 1900
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39

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gacttcatcc agcagcaccg ccaggctctg gagtcggagt atgtgtctgc 1950

acacctacac gagtggatcg acctcatctt tggctacaag cagcgggggc 2000

cagccgccga ggaggccctc aatgtcttct attactgcac ctatgagggg 2050

gctgtagacc tggaccatgt gacagatgag cgggaacgga aggctctgga 2100

gggcattatc agcaactttg ggcagactcc ctgtcagctg ctgaaggagc 2150

cacatccaac tcggctctca gctgaggaag cagcccatcg ccttgcacgc 2200

ctggacacta actcacctag catcttccag cacctggacg aactcaaggc 2250

attcttcgca gaggtgactg tgagtgccag tgggctgctg ggcacccaca 2300

gctggttgcc ctatgaccgc aacataagca actacttcag cttcagcaaa 2350

gaccccacca tgggcagcca caagacgcag cgactgctga gtggcccgtg 2400

ggtgccaggc agtggtgtga gtggacaagc actggcagtg ccccggatg 2450

gaaagctgct attcagcggt ggccactggg atggcagcct gcgggtgact 2500

gcactacccc gtggcaagct gttgagccag ctcagctgcc accttgatgt 2550

agtaacctgc cttgcactgg acacctgtgg catctacctc atctcaggct 2600

cccgggacac cacgtgcatg gtgtggcggc tcctgcatca gggtggtctg 2650

tcagtaggcc tggcaccaaa gcctgtgcag gtcctgtatg ggcatggggc 2700

tgcagtgagc tgtgtggcca tcagcactga acttgacatg gctgtgtctg 2750

gatctgagga tggaactgtg atcatacaca ctgtacgccg cggacagttt 2800

gtagcggcac tacggcctct gggtgccaca ttccctggac ctattttcca 2850

cctggcattg gggtccgaag gccagattgt ggtacagagc tcagcgtggg 2900

aacgtcctgg ggcccaggtc acctactcct tgcacctgta ttcagtcaat 2950

gggaagttgc gggcttcact gcccctggca gagcagccta cagccctgac 3000

ggtgacagag gactttgtgt tgctgggcac cgcccagtgc gccctgcaca 3050

tcctccaact aaacacactg ctcccggccg cgcctccctt gcccatgaag 3100

gtggccatcc gcagcgtggc cgtgaccaag gagcgcagcc acgtgctggt 3150

gggcctggag gatggcaagc tcatcgtggt ggtcgcgggg cagccctctg 3200

aggtgcgcag cagccagttc gcgcggaagc tgtggcggtc ctcgcggcgc 3250

atctcccagg tgtcctcggg agagacggaa tacaacccta ctgaggcgcg 3300

ctgaacctgg ccagtccggc tgctcgggcc ccgcccccgg caggcctggc 3350
```

40

```
            ccgggaggcc ccgcccagaa gtcggcggga acaccccggg gtgggcagcc 3400

            caggggtga gcggggccca ccctgcccag ctcagggatt ggcgggcgat 3450

            gttacccct caggggttgg cgggcggaag tcccgcccct cgccggctga 3500

            ggggccgccc tgagggccag cactggcgtc t 3531
```

<210> 33
<211> 1003
<212> PRT
<213> Homo sapiens

<400> 33
```
 Met Ser Gln Phe Glu Met Asp Thr Tyr Ala Lys Ser His Asp Leu
   1               5                  10                  15

 Met Ser Gly Phe Trp Asn Ala Cys Tyr Asp Met Leu Met Ser Ser
                  20                  25                  30

     Gly Gln Arg Arg Gln Trp Glu Arg Ala Gln Ser Arg Arg Ala Phe
                      35                  40                  45

     Gln Glu Leu Val Leu Glu Pro Ala Gln Arg Arg Ala Arg Leu Glu
                      50                  55                  60

     Gly Leu Arg Tyr Thr Ala Val Leu Lys Gln Gln Ala Thr Gln His
                      65                  70                  75

     Ser Met Ala Leu Leu His Trp Gly Ala Leu Trp Arg Gln Leu Ala
                      80                  85                  90

     Ser Pro Cys Gly Ala Trp Ala Leu Arg Asp Thr Pro Ile Pro Arg
                      95                 100                 105

     Trp Lys Leu Ser Ser Ala Glu Thr Tyr Ser Arg Met Arg Leu Lys
                     110                 115                 120

     Leu Val Pro Asn His His Phe Asp Pro His Leu Glu Ala Ser Ala
                     125                 130                 135

     Leu Arg Asp Asn Leu Gly Glu Val Pro Leu Thr Pro Thr Glu Glu
                     140                 145                 150

     Ala Ser Leu Pro Leu Ala Val Thr Lys Glu Ala Lys Val Ser Thr
                     155                 160                 165

     Pro Pro Glu Leu Leu Gln Glu Asp Gln Leu Gly Glu Asp Glu Leu
                     170                 175                 180

     Ala Glu Leu Glu Thr Pro Met Glu Ala Ala Glu Leu Asp Glu Gln
                     185                 190                 195

     Arg Glu Lys Leu Val Leu Ser Ala Glu Cys Gln Leu Val Thr Val
                     200                 205                 210

     Val Ala Val Val Pro Gly Leu Leu Glu Val Thr Thr Gln Asn Val
                     215                 220                 225
```

41

Tyr Phe Tyr Asp Gly Ser Thr Glu Arg Val Glu Thr Glu Glu Gly
                230   235   240

Ile Gly Tyr Asp Phe Arg Arg Pro Leu Ala Gln Leu Arg Glu Val
                245   250   255

His Leu Arg Arg Phe Asn Leu Arg Arg Ser Ala Leu Glu Leu Phe
                260   265   270

Phe Ile Asp Gln Ala Asn Tyr Phe Leu Asn Phe Pro Cys Lys Val
                275   280   285

Gly Thr Thr Pro Val Ser Ser Pro Ser Gln Thr Pro Arg Pro Gln
                290   295   300

Pro Gly Pro Ile Pro Pro His Thr Gln Val Arg Asn Gln Val Tyr
                305   310   315

Ser Trp Leu Leu Arg Leu Arg Pro Pro Ser Gln Gly Tyr Leu Ser
                320   325   330

Ser Arg Ser Pro Gln Glu Met Leu Arg Ala Ser Gly Leu Thr Gln
                335   340   345

Lys Trp Val Gln Arg Glu Ile Ser Asn Phe Glu Tyr Leu Met Gln
                350   355   360

Leu Asn Thr Ile Ala Gly Arg Thr Tyr Asn Asp Leu Ser Gln Tyr
                365   370   375

Pro Val Phe Pro Trp Val Leu Gln Asp Tyr Val Ser Pro Thr Leu
                380   385   390

Asp Leu Ser Asn Pro Ala Val Phe Arg Asp Leu Ser Lys Pro Ile
                395   400   405

Gly Val Val Asn Pro Lys His Ala Gln Leu Val Arg Glu Lys Tyr
                410   415   420

Glu Ser Phe Glu Asp Pro Ala Gly Thr Ile Asp Lys Phe His Tyr
                425   430   435

Gly Thr His Tyr Ser Asn Ala Ala Gly Val Met His Tyr Leu Ile
                440   445   450

Arg Val Glu Pro Phe Thr Ser Leu His Val Gln Leu Gln Ser Gly
                455   460   465

Arg Phe Asp Cys Ser Asp Arg Gln Phe His Ser Val Ala Ala Ala
                470   475   480

Trp Gln Ala Arg Leu Glu Ser Pro Ala Asp Val Lys Glu Leu Ile
                485   490   495

Pro Glu Phe Phe Tyr Phe Pro Asp Phe Leu Glu Asn Gln Asn Gly
                500   505   510

Phe Asp Leu Gly Cys Leu Gln Leu Thr Asn Glu Lys Val Gly Asp

42

```
                515                    520                    525
Val Val Leu Pro Pro Trp Ala Ser Ser Pro Glu Asp Phe Ile Gln
            530                    535                    540
Gln His Arg Gln Ala Leu Glu Ser Glu Tyr Val Ser Ala His Leu
            545                    550                    555
His Glu Trp Ile Asp Leu Ile Phe Gly Tyr Lys Gln Arg Gly Pro
            560                    565                    570
Ala Ala Glu Glu Ala Leu Asn Val Phe Tyr Tyr Cys Thr Tyr Glu
            575                    580                    585
Gly Ala Val Asp Leu Asp His Val Thr Asp Glu Arg Glu Arg Lys
            590                    595                    600
Ala Leu Glu Gly Ile Ile Ser Asn Phe Gly Gln Thr Pro Cys Gln
            605                    610                    615
Leu Leu Lys Glu Pro His Pro Thr Arg Leu Ser Ala Glu Glu Ala
            620                    625                    630
Ala His Arg Leu Ala Arg Leu Asp Thr Asn Ser Pro Ser Ile Phe
            635                    640                    645
Gln His Leu Asp Glu Leu Lys Ala Phe Phe Ala Glu Val Thr Val
            650                    655                    660
Ser Ala Ser Gly Leu Leu Gly Thr His Ser Trp Leu Pro Tyr Asp
            665                    670                    675
Arg Asn Ile Ser Asn Tyr Phe Ser Phe Ser Lys Asp Pro Thr Met
            680                    685                    690
Gly Ser His Lys Thr Gln Arg Leu Leu Ser Gly Pro Trp Val Pro
            695                    700                    705
Gly Ser Gly Val Ser Gly Gln Ala Leu Ala Val Ala Pro Asp Gly
            710                    715                    720
Lys Leu Leu Phe Ser Gly Gly His Trp Asp Gly Ser Leu Arg Val
            725                    730                    735
Thr Ala Leu Pro Arg Gly Lys Leu Leu Ser Gln Leu Ser Cys His
            740                    745                    750
Leu Asp Val Val Thr Cys Leu Ala Leu Asp Thr Cys Gly Ile Tyr
            755                    760                    765
Leu Ile Ser Gly Ser Arg Asp Thr Thr Cys Met Val Trp Arg Leu
            770                    775                    780
Leu His Gln Gly Gly Leu Ser Val Gly Leu Ala Pro Lys Pro Val
            785                    790                    795
Gln Val Leu Tyr Gly His Gly Ala Ala Val Ser Cys Val Ala Ile
            800                    805                    810
```

43

```
Ser Thr Glu Leu Asp Met Ala Val Ser Gly Ser Glu Asp Gly Thr
             815                 820                 825

Val Ile Ile His Thr Val Arg Arg Gly Gln Phe Val Ala Ala Leu
             830                 835                 840

Arg Pro Leu Gly Ala Thr Phe Pro Gly Pro Ile Phe His Leu Ala
             845                 850                 855

Leu Gly Ser Glu Gly Gln Ile Val Val Gln Ser Ser Ala Trp Glu
             860                 865                 870

Arg Pro Gly Ala Gln Val Thr Tyr Ser Leu His Leu Tyr Ser Val
             875                 880                 885

Asn Gly Lys Leu Arg Ala Ser Leu Pro Leu Ala Glu Gln Pro Thr
             890                 895                 900

Ala Leu Thr Val Thr Glu Asp Phe Val Leu Leu Gly Thr Ala Gln
             905                 910                 915

Cys Ala Leu His Ile Leu Gln Leu Asn Thr Leu Leu Pro Ala Ala
             920                 925                 930

Pro Pro Leu Pro Met Lys Val Ala Ile Arg Ser Val Ala Val Thr
             935                 940                 945

Lys Glu Arg Ser His Val Leu Val Gly Leu Glu Asp Gly Lys Leu
             950                 955                 960

Ile Val Val Val Ala Gly Gln Pro Ser Glu Val Arg Ser Ser Gln
             965                 970                 975

Phe Ala Arg Lys Leu Trp Arg Ser Ser Arg Arg Ile Ser Gln Val
             980                 985                 990

Ser Ser Gly Glu Thr Glu Tyr Asn Pro Thr Glu Ala Arg
             995                 1000
```

<210> 34
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
 tgactgcact accccgtggc aagctgttga gccagctcag ctg 43

<210> 35
<211> 1395
<212> DNA
<213> Homo sapiens

<400> 35
 cggacgcgtg ggcggacgcg tggggggctgt gagaaagtgc caataaatac 50

44

```
atcatgcaac cccacggccc accttgtgaa ctcctcgtgc ccagggctga 100

tgtgcgtctt ccagggctac tcatccaaag gcctaatcca acgttctgtc 150

ttcaatctgc aaatctatgg ggtcctgggg ctcttctgga cccttaactg 200

ggtactggcc ctgggccaat gcgtcctcgc tggagccttt gcctccttct 250

actgggcctt ccacaagccc caggacatcc ctaccttccc cttaatctct 300

gccttcatcc gcacactccg ttaccacact gggtcattgg catttggagc 350

cctcatcctg acccttgtgc agatagcccg ggtcatcttg gagtatattg 400

accacaagct cagaggagtg cagaaccctg tagcccgctg catcatgtgc 450

tgtttcaagt gctgcctctg gtgtctggaa aaatttatca agttcctaaa 500

ccgcaatgca tacatcatga tcgccatcta cgggaagaat ttctgtgtct 550

cagccaaaaa tgcgttcatg ctactcatgc gaaacattgt cagggtggtc 600

gtcctggaca aagtcacaga cctgctgctg ttctttggga agctgctggt 650

ggtcggaggc gtggggtcc tgtccttctt ttttttctcc ggtcgcatcc 700

cggggctggg taaagacttt aagagccccc acctcaacta ttactggctg 750

cccatcatga cctccatcct gggggcctat gtcatcgcca gcggcttctt 800

cagcgttttc ggcatgtgtg tggacacgct cttcctctgc ttcctggaag 850

acctggagcg gaacaacggc tccctggacc ggccctacta catgtccaag 900

agccttctaa agattctggg caagaagaac gaggcgcccc cggacaacaa 950

gaagaggaag aagtgacagc tccggccctg atccaggact gcaccccacc 1000

cccaccgtcc agccatccaa cctcacttcg ccttacaggt ctccattttg 1050

tggtaaaaaa aggttttagg ccaggcgccg tggctcacgc ctgtaatcca 1100

acactttgag aggctgaggc gggcggatca cctgagtcag gagttcgaga 1150

ccagcctggc caacatggtg aaacctccgt ctctattaaa aatacaaaaa 1200

ttagccgaga gtggtggcat gcacctgtca tcccagctac tcgggaggct 1250

gaggcaggag aatcgcttga acccgggagg cagaggttgc agtgagccga 1300

gatcgcgcca ctgcactcca acctgggtga cagactctgt ctccaaaaca 1350

aaacaaacaa acaaaaagat tttattaaag atattttgtt aactc 1395
```

<210> 36
<211> 321
<212> PRT
<213> Homo sapiens

<400> 36

```
Arg Thr Arg Gly Arg Thr Arg Gly Gly Cys Glu Lys Val Pro Ile
 1               5                  10                      15

Asn Thr Ser Cys Asn Pro Thr Ala His Leu Val Asn Ser Ser Cys
               20                  25                      30

Pro Gly Leu Met Cys Val Phe Gln Gly Tyr Ser Ser Lys Gly Leu
               35                  40                      45

Ile Gln Arg Ser Val Phe Asn Leu Gln Ile Tyr Gly Val Leu Gly
               50                  55                      60

Leu Phe Trp Thr Leu Asn Trp Val Leu Ala Leu Gly Gln Cys Val
               65                  70                      75

Leu Ala Gly Ala Phe Ala Ser Phe Tyr Trp Ala Phe His Lys Pro
               80                  85                      90

Gln Asp Ile Pro Thr Phe Pro Leu Ile Ser Ala Phe Ile Arg Thr
               95                  100                     105

Leu Arg Tyr His Thr Gly Ser Leu Ala Phe Gly Ala Leu Ile Leu
               110                 115                     120

Thr Leu Val Gln Ile Ala Arg Val Ile Leu Glu Tyr Ile Asp His
               125                 130                     135

Lys Leu Arg Gly Val Gln Asn Pro Val Ala Arg Cys Ile Met Cys
               140                 145                     150

Cys Phe Lys Cys Cys Leu Trp Cys Leu Glu Lys Phe Ile Lys Phe
               155                 160                     165

Leu Asn Arg Asn Ala Tyr Ile Met Ile Ala Ile Tyr Gly Lys Asn
               170                 175                     180

Phe Cys Val Ser Ala Lys Asn Ala Phe Met Leu Leu Met Arg Asn
               185                 190                     195

Ile Val Arg Val Val Val Leu Asp Lys Val Thr Asp Leu Leu Leu
               200                 205                     210

Phe Phe Gly Lys Leu Leu Val Val Gly Gly Val Gly Val Leu Ser
               215                 220                     225

Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly Leu Gly Lys Asp Phe
               230                 235                     240

Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro Ile Met Thr Ser
               245                 250                     255

Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe Ser Val Phe
               260                 265                     270

Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu Asp Leu
               275                 280                     285
```

46

Glu Arg Asn Asn Gly Ser Leu Asp Arg Pro Tyr Tyr Met Ser Lys
                290   295   300

Ser Leu Leu Lys Ile Leu Gly Lys Lys Asn Glu Ala Pro Pro Asp
                305   310   315

Asn Lys Lys Arg Lys Lys
                320

<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
 tcgtgcccag gggctgatgt gc 22

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
 gtctttaccc agccccggga tgcg 24

<210> 39
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
 ggcctaatcc aacgttctgt cttcaatctg caaatctatg gggtcctggg 50

<210> 40
<211> 1365
<212> DNA
<213> Homo sapiens

<400> 40
 gagtcttgac cgccgccggg ctcttggtac ctcagcgcga gcgccaggcg 50

 tccggccgcc gtggctatgt tcgtgtccga tttccgcaaa gagttctacg 100

 aggtggtcca gagccagagg gtccttctct tcgtggcctc ggacgtggat 150

 gctctgtgtg cgtgcaagat ccttcaggcc ttgttccagt gtgaccacgt 200

 gcaatatacg ctggttccag tttctgggtg gcaagaactt gaaactgcat 250

```
ttcttgagca taaagaacag tttcattatt ttattctcat aaactgtgga 300

gctaatgtag acctattgga tattcttcaa cctgatgaag acactatatt 350

ctttgtgtgt gactcccata ggccagtcaa tgtcgtcaat gtatacaacg 400

atacccagat caaattactc attaaacaag atgatgacct tgaagttccc 450

gcctatgaag acatcttcag ggatgaagag gaggatgaag agcattcagg 500

aaatgacagt gatgggtcag agccttctga gaagcgcaca cggttagaag 550

aggagatagt ggagcaaacc atgcggagga ggcagcggcg agagtgggag 600

gcccggagaa gagacatcct ctttgactac gagcagtatg aatatcatgg 650

gacatcgtca gccatggtga tgtttgagct ggcttggatg ctgtccaagg 700

acctgaatga catgctgtgg tgggccatcg ttggactaac agaccagtgg 750

gtgcaagaca agatcactca aatgaaatac gtgactgatg ttggtgtcct 800

gcagcgccac gtttcccgcc acaaccaccg gaacgaggat gaggagaaca 850

cactctccgt ggactgcaca cggatctcct ttgagtatga cctccgcctg 900

gtgctctacc agcactggtc cctccatgac agcctgtgca acaccagcta 950

taccgcagcc aggttcaagc tgtggtctgt gcatggacag aagcggctcc 1000

aggagttcct tgcagacatg ggtcttcccc tgaagcaggt gaagcagaag 1050

ttccaggcca tggacatctc cttgaaggag aatttgcggg aaatgattga 1100

agagtctgca aataaatttg ggatgaagga catgcgcgtg cagactttca 1150

gcattcattt tgggttcaag cacaagtttc tggccagcga cgtggtcttt 1200

gccaccatgt ctttgatgga gagccccgag aaggatggct cagggacaga 1250

tcacttcatc caggctctgg acagcctctc caggagtaac ctggacaagc 1300

tgtaccatgg cctggaactc gccaagaagc agctgcgagc cacccagcag 1350

accattgcca gctgc 1365
```

```
<210> 41
<211> 566
<212> PRT
<213> Homo sapiens

<400> 41
Met Phe Val Ser Asp Phe Arg Lys Glu Phe Tyr Glu Val Val Gln
 1               5                  10                  15

Ser Gln Arg Val Leu Leu Phe Val Ala Ser Asp Val Asp Ala Leu
                20                  25                  30
```

48

```
Cys Ala Cys Lys Ile Leu Gln Ala Leu Phe Gln Cys Asp His Val
            35              40              45

Gln Tyr Thr Leu Val Pro Val Ser Gly Trp Gln Glu Leu Glu Thr
            50              55              60

Ala Phe Leu Glu His Lys Glu Gln Phe His Tyr Phe Ile Leu Ile
            65              70              75

Asn Cys Gly Ala Asn Val Asp Leu Leu Asp Ile Leu Gln Pro Asp
            80              85              90

Glu Asp Thr Ile Phe Phe Val Cys Asp Ser His Arg Pro Val Asn
            95              100             105

Val Val Asn Val Tyr Asn Asp Thr Gln Ile Lys Leu Leu Ile Lys
            110             115             120

Gln Asp Asp Asp Leu Glu Val Pro Ala Tyr Glu Asp Ile Phe Arg
            125             130             135

Asp Glu Glu Glu Asp Glu Glu His Ser Gly Asn Asp Ser Asp Gly
            140             145             150

Ser Glu Pro Ser Glu Lys Arg Thr Arg Leu Glu Glu Glu Ile Val
            155             160             165

Glu Gln Thr Met Arg Arg Arg Gln Arg Arg Glu Trp Glu Ala Arg
            170             175             180

Arg Arg Asp Ile Leu Phe Asp Tyr Glu Gln Tyr Glu Tyr His Gly
            185             190             195

Thr Ser Ser Ala Met Val Met Phe Glu Leu Ala Trp Met Leu Ser
            200             205             210

Lys Asp Leu Asn Asp Met Leu Trp Trp Ala Ile Val Gly Leu Thr
            215             220             225

Asp Gln Trp Val Gln Asp Lys Ile Thr Gln Met Lys Tyr Val Thr
            230             235             240

Asp Val Gly Val Leu Gln Arg His Val Ser Arg His Asn His Arg
            245             250             255

Asn Glu Asp Glu Glu Asn Thr Leu Ser Val Asp Cys Thr Arg Ile
            260             265             270

Ser Phe Glu Tyr Asp Leu Arg Leu Val Leu Tyr Gln His Trp Ser
            275             280             285

Leu His Asp Ser Leu Cys Asn Thr Ser Tyr Thr Ala Ala Arg Phe
            290             295             300

Lys Leu Trp Ser Val His Gly Gln Lys Arg Leu Gln Glu Phe Leu
            305             310             315

Ala Asp Met Gly Leu Pro Leu Lys Gln Val Lys Gln Lys Phe Gln
```

Ala Met Asp Ile Ser Leu Lys Glu Asn Leu Arg Glu Met Ile Glu
                335   340   345

Glu Ser Ala Asn Lys Phe Gly Met Lys Asp Met Arg Val Gln Thr
                350   355   360

Phe Ser Ile His Phe Gly Phe Lys His Lys Phe Leu Ala Ser Asp
                365   370   375

Val Val Phe Ala Thr Met Ser Leu Met Glu Ser Pro Glu Lys Asp
                380   385   390

Gly Ser Gly Thr Asp His Phe Ile Gln Ala Leu Asp Ser Leu Ser
                395   400   405

Arg Ser Asn Leu Asp Lys Leu Tyr His Gly Leu Glu Leu Ala Lys
                410   415   420

Lys Gln Leu Arg Ala Thr Gln Gln Thr Ile Ala Ser Cys Leu Cys
                425   430   435

Thr Asn Leu Val Ile Ser Gln Gly Pro Phe Leu Tyr Cys Ser Leu
                440   445   450

Met Glu Gly Thr Pro Asp Val Met Leu Phe Ser Arg Pro Ala Ser
                455   460   465

Leu Ser Leu Leu Ser Lys His Leu Leu Lys Ser Phe Val Cys Ser
                470   475   480

Thr Lys Asn Arg Arg Cys Lys Leu Leu Pro Leu Val Met Ala Ala
                485   490   495

Pro Leu Ser Met Glu His Gly Thr Val Thr Val Val Gly Ile Pro
                500   505   510

Pro Glu Thr Asp Ser Ser Asp Arg Lys Asn Phe Phe Gly Arg Ala
                515   520   525

Phe Glu Lys Ala Ala Glu Ser Thr Ser Ser Arg Met Leu His Asn
                530   535   540

His Phe Asp Leu Ser Val Ile Glu Leu Lys Ala Glu Asp Arg Ser
                545   550   555

Lys Phe Leu Asp Ala Leu Ile Ser Leu Leu Ser
                560   565

<210> 42
<211> 380
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 44, 118, 172, 183

<223> unknown base

<400> 42
gtacctcagc gcgagcgcca ggcgtccggc cgccgtggct atgntcgtgt 50

ccgatttccg caaagagttc tacgaggtgg tccagagcca gagggtcctt 100

ctcttcgtgg cctcggangt ggatgctctg tgtgcgtgca agatccttca 150

ggccttgttc cagtgtgacc angtgcaata tangctggtt ccagtttctg 200

ggtggcaaga acttgaaact gcatttcttg agcataaaga acagtttcat 250

tattttattc tcataaactg tggagctaat gtagacctat tggatattct 300

tcaacctgat gaagacacta tattctttgt gtgtgacacc cataggccag 350

tcaatgttgt caatgtatac aacgataccc 380

<210> 43
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ttccgcaaag agttctacga ggtgg 25

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
attgacaaca ttgactggcc tatggg 26

<210> 45
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
gtggatgctc tgtgtgcgtg caagatcctt caggccttgt tccagtgtga 50

<210> 46
<211> 3089
<212> DNA
<213> Homo sapiens

<400> 46

51

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caggaaccct ctctttgggt ctggattggg acccctttcc agtaccattt 50

tttctagtga accacgaagg gacgatacca gaaaacaccc tcaacccaaa 100

ggaaatagac tacagcccca attggctgac tttggctata gaaaaaagaa 150

aggaacgaaa agagacagtt tttttggaa agctaagtct tccctttatc 200

gagtcaagaa acccccctt cttgagctat ttacagcttt taacaattga 250

gtaaagtacg ctccggtcac catggtgaca gccgccctgg gtcccgtctg 300

ggcagcgctc ctgctctttc tcctgatgtg tgagatccgt atggtggagc 350

tcacctttga cagagctgtg gccagcggct gccaacggtg ctgtgactct 400

gaggacccc tggatcctgc ccatgtatcc tcagcctctt cctccggccg 450

cccccacgcc ctgcctgaga tcagaccct cattaatatc accatcctga 500

agggtgacaa aggggaccca ggcccaatgg gcctgccagg gtacatgggc 550

agggagggtc cccaagggga gcctggccct cagggcagca agggtgacaa 600

gggggagatg ggcagccccg gcgccccgtg ccagaagcgc ttcttcgcct 650

tctcagtggg ccgcaagacg gccctgcaca gcggcgagga cttccagacg 700

ctgctcttcg aaagggtctt tgtgaacctt gatgggtgct ttgacatggc 750

gaccggccag tttgctgctc ccctgcgtgg catctacttc ttcagcctca 800

atgtgcacag ctggaattac aaggagacgt acgtgcacat tatgcataac 850

cagaaagagg ctgtcatcct gtacgcgcag cccagcgagc gcagcatcat 900

gcagagccag agtgtgatgc tggacctggc ctacggggac cgcgtctggg 950

tgcggctctt caagcgccag cgcgagaacg ccatctacag caacgacttc 1000

gacacctaca tcaccttcag cggccacctc atcaaggccg aggacgactg 1050

agggcctctg ggccaccctc ccggctggag agctcaggtg ctggtcccgt 1100

cccctgcagg gctcagtttg cactgctgtg aagcaggaag gccagggagg 1150

tccccgggga cctggcattc tggggagacc ctgcttctat cttggctgcc 1200

atcatccctc ccagcctatt tctgctcctc tcttctctct tggacctatt 1250

ttaagaagct tgctaaccta aatattctag aactttccca gcctcgtagc 1300

ccagcacttc tcaaacttgg aaatgcatgc gaatcacccg gggttcgtgt 1350

taaatgcaga ttctgactca gcaggtctga gtgggtccag gattctgtgt 1400

ttctcatatg ttcctgggtg atgctgatgg ggtcagtcta tgaaccacac 1450
```

52

```
tggagcaacc aggttctagg actttctcaa tattctagta ctttctgaac 1500

attctggaat cctccccaca ttctagaatt ctcccaacat ttttttttct 1550

tgagacagag tcttgctctg ttgcccaggc tagagtgcag tggtgcaatc 1600

tcagttcact gcaacctctg cctcccgggt tcaagcgatt cttctgcctc 1650

agcctcccta gtggctggga ttacaggcgc ctgctaccat gcctggctaa 1700

tttttgtatt tttagtagag atggggtttc accatattgg ccaggctggt 1750

cttgaactcc tgacttcagg tgacccaccc gcctcggcct ctcaaaatgc 1800

tgggattaca ggtgtgagcc accgtgcctg gccaattcca acattcttaa 1850

attctctcat ccctccaggg ctccccgtgc tatgttctct ttaccccttc 1900

cccctcttct cttgctcagg cctgcaccac tgcagccacc gttcatttat 1950

tcattcatta aacactgagc actcactctg tgctgggtcc cgggaagggt 2000

gagggggtca gacacaggcc ctgcccctgc cctcagtgac tggccagtcc 2050

agcccaggcg gggagagatg tgtacatagg ttttaaagca gacccagagc 2100

tcatgggggc ctgtgttctg ggtgttcagg tgctgctggt cctccattac 2150

ccactgctcc ccaaggctgg tgggacgggg tcccggtggc aggggcaggt 2200

atctccttcc cgttcctcat ccacctgccc agtgctcatc gttacagcaa 2250

accccagggg gccttggcca ggtcaagggt tctgtgagga gaggacccag 2300

gagtgtgggg gcatttgggg ggtgaagtgg cccccgaaga atggaaccca 2350

cacccatagc tctccccaca gctgatacgg catcctgcga gaagacctgc 2400

cctcctcact gggatcccct tcctgcctcc tcccagggct ctgccagggc 2450

cttgctcagt cccttccacc aaagtcatct gaacttccgt ttccccaggg 2500

cctccagctg ccctcagaca ctgatgtctg tccccaggtg ctctctgccc 2550

ctcatgcccc tctcaccggc ccagtgcccc gactctccag gctttatcaa 2600

ggtgctaagg cccgggtggg cagctcctcg tctcagagcc ctcctccggc 2650

ctggtgctgc ctttacaaac acctgcagga gaagggccac ggaagcccca 2700

ggctttagag ccctcagcag gtctggggag ctagagcaaa ggagggacct 2750

caggccttcc gtttcttctt ccagggtggg gtggcctggt gttcccctag 2800

ccttccaaac ccaggtggcc tgcccttctc cccagaggga ggcggcctcc 2850

gcccattggt gctcatgcag actctggggc tgaggtgccc cggggggtga 2900
```

53

```
tctctggtgc tcacagccga gggagccgtg gctccatggc cagatgacgg 2950

aaacagggtc tgaccaagtg ccaggaagac ctgtgctata aaccaccctg 3000

cctgatcctg cccctgcctg accccgccac gccctgccgt ccagcatgat 3050

taaagaatgc tgtctcctct tggaaaaaaa aaaaaaaaa 3089
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<210> 47
<211> 259
<212> PRT
<213> Homo sapiens

<220>
<221> Signal Peptide
<222> 1-20
<223> Signal Peptide

<220>
<221> N-glycosylation Site
<222> 72-75
<223> N-glycosylation Site

<220>
<221> C1q Domain Proteins
<222> 144-178, 78-111, 84-117
<223> C1q Domain Proteins

<400> 47
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Met Val Thr Ala Ala Leu Gly Pro Val Trp Ala Ala Leu Leu Leu
 1               5                   10                  15

Phe Leu Leu Met Cys Glu Ile Arg Met Val Glu Leu Thr Phe Asp
               20                  25                  30

Arg Ala Val Ala Ser Gly Cys Gln Arg Cys Cys Asp Ser Glu Asp
               35                  40                  45

Pro Leu Asp Pro Ala His Val Ser Ser Ala Ser Ser Ser Gly Arg
           50                  55                  60

Pro His Ala Leu Pro Glu Ile Arg Pro Tyr Ile Asn Ile Thr Ile
           65                  70                  75

Leu Lys Gly Asp Lys Gly Asp Pro Gly Pro Met Gly Leu Pro Gly
           80                  85                  90

Tyr Met Gly Arg Glu Gly Pro Gln Gly Glu Pro Gly Pro Gln Gly
           95                  100                 105

Ser Lys Gly Asp Lys Gly Glu Met Gly Ser Pro Gly Ala Pro Cys
           110                 115                 120

Gln Lys Arg Phe Phe Ala Phe Ser Val Gly Arg Lys Thr Ala Leu
           125                 130                 135

His Ser Gly Glu Asp Phe Gln Thr Leu Leu Phe Glu Arg Val Phe
               140                 145                 150
```

54

```
Val Asn Leu Asp Gly Cys Phe Asp Met Ala Thr Gly Gln Phe Ala
            155             160                 165

Ala Pro Leu Arg Gly Ile Tyr Phe Phe Ser Leu Asn Val His Ser
            170             175                 180

Trp Asn Tyr Lys Glu Thr Tyr Val His Ile Met His Asn Gln Lys
            185             190                 195

Glu Ala Val Ile Leu Tyr Ala Gln Pro Ser Glu Arg Ser Ile Met
            200             205                 210

Gln Ser Gln Ser Val Met Leu Asp Leu Ala Tyr Gly Asp Arg Val
            215             220                 225

Trp Val Arg Leu Phe Lys Arg Gln Arg Glu Asn Ala Ile Tyr Ser
            230             235                 240

Asn Asp Phe Asp Thr Tyr Ile Thr Phe Ser Gly His Leu Ile Lys
            245             250                 255

Ala Glu Asp Asp


<210> 48
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
 ccagacgctg ctcttcgaaa gggtc 25

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
 ggtccccgta ggccaggtcc agc 23

<210> 50
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
 ctacttcttc agcctcaatg tgcacagctg gaattacaag gagacgtacg 50

<210> 51
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55

<211> 2768
<212> DNA
<213> Homo sapiens

<400> 51
actcgaacgc agttgcttcg ggacccagga ccccctcggg cccgacccgc 50

caggaaagac tgaggccgcg gcctgccccg cccggctccc tgcgccgccg 100

ccgcctcccg ggacagaaga tgtgctccag ggtccctctg ctgctgccgc 150

tgctcctgct actggccctg gggcctgggg tgcagggctg cccatccggc 200

tgccagtgca gccagccaca gacagtcttc tgcactgccc gccaggggac 250

cacggtgccc cgagacgtgc cacccgacac ggtggggctg tacgtctttg 300

agaacggcat caccatgctc gacgcaggca gctttgccgg cctgccgggc 350

ctgcagctcc tggacctgtc acagaaccag atcgccagcc tgcccagcgg 400

ggtcttccag ccactcgcca acctcagcaa cctggacctg acggccaaca 450

ggctgcatga aatcaccaat gagaccttcc gtggcctgcg gcgcctcgag 500

cgcctctacc tgggcaagaa ccgcatccgc cacatccagc ctggtgcctt 550

cgacacgctc gaccgcctcc tggagctcaa gctgcaggac aacgagctgc 600

gggcactgcc cccgctgcgc ctgccccgcc tgctgctgct ggacctcagc 650

cacaacagcc tcctggccct ggagcccggc atcctggaca ctgccaacgt 700

ggaggcgctg cggctggctg gtctggggct gcagcagctg gacgaggggc 750

tcttcagccg cttgcgcaac ctccacgacc tggatgtgtc cgacaaccag 800

ctggagcgag tgccacctgt gatccgaggc ctccggggcc tgacgcgcct 850

gcggctggcc ggcaacaccc gcattgccca gctgcggccc gaggacctgg 900

ccggcctggc tgccctgcag gagctggatg tgagcaacct aagcctgcag 950

gccctgcctg gcgacctctc gggcctcttc cccgcctgc ggctgctggc 1000

agctgcccgc aacccccttca actgcgtgtg cccctgagc tggtttggcc 1050

cctgggtgcg cgagagccac gtcacactgg ccagccctga ggagacgcgc 1100

tgccacttcc cgcccaagaa cgctggccgg ctgctcctgg agcttgacta 1150

cgccgacttt ggctgcccag ccaccaccac cacagccaca gtgcccacca 1200

cgaggcccgt ggtgcgggag cccacagcct tgtcttctag cttggctcct 1250

acctggctta gccccacagc gccggccact gaggccccca gccgccctc 1300

cactgcccca ccgactgtag ggcctgtccc ccagccccag gactgcccac 1350

56

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cgtccacctg cctcaatggg ggcacatgcc acctggggac acggcaccac 1400

ctggcgtgct tgtgccccga aggcttcacg ggcctgtact gtgagagcca 1450

gatggggcag gggacacggc ccagccctac accagtcacg ccgaggccac 1500

cacggtccct gaccctgggc atcgagccgg tgagccccac ctccctgcgc 1550

gtggggctgc agcgctacct ccaggggagc tccgtgcagc tcaggagcct 1600

ccgtctcacc tatcgcaacc tatcgggccc tgataagcgg ctggtgacgc 1650

tgcgactgcc tgcctcgctc gctgagtaca cggtcaccca gctgcggccc 1700

aacgccactt actccgtctg tgtcatgcct ttggggcccg ggcgggtgcc 1750

ggagggcgag gaggcctgcg gggaggccca tacaccccca gccgtccact 1800

ccaaccacgc cccagtcacc caggcccgcg agggcaacct gccgctcctc 1850

attgcgcccg ccctggccgc ggtgctcctg gccgcgctgg ctgcggtggg 1900

ggcagcctac tgtgtgcggc gggggcgggc catggcagca gcggctcagg 1950

acaaagggca ggtggggcca ggggctgggc ccctggaact ggagggagtg 2000

aaggtcccct tggagccagg cccgaaggca acagagggcg gtggagaggc 2050

cctgcccagc gggtctgagt gtgaggtgcc actcatgggc ttcccagggc 2100

ctggcctcca gtcacccctc cacgcaaagc cctacatcta agccagagag 2150

agacagggca gctggggccg ggctctcagc cagtgagatg gccagccccc 2200

tcctgctgcc acaccacgta agttctcagt cccaacctcg gggatgtgtg 2250

cagacagggc tgtgtgacca cagctgggcc ctgttccctc tggacctcgg 2300

tctcctcatc tgtgagatgc tgtggcccag ctgacgagcc ctaacgtccc 2350

cagaaccgag tgcctatgag gacagtgtcc gccctgccct ccgcaacgtg 2400

cagtccctgg gcacggcggg ccctgccatg tgctggtaac gcatgcctgg 2450

gtcctgctgg gctctcccac tccaggcgga ccctgggggc cagtgaagga 2500

agctcccgga aagagcagag ggagagcggg taggcggctg tgtgactcta 2550

gtcttggccc caggaagcga aggaacaaaa gaaactggaa aggaagatgc 2600

tttaggaaca tgttttgctt ttttaaaata tatatattta taagagatcc 2650

tttcccattt attctgggaa gatgtttttc aaactcagag acaaggactt 2700

tggtttttgt aagacaaacg atgatatgaa ggccttttgt aagaaaaaat 2750

aaaagatgaa gtgtgaaa 2768
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57

<210> 52
<211> 673
<212> PRT
<213> Homo sapiens

<400> 52

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Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu Leu
  1               5                  10                  15

Ala Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys
                 20                  25                  30

Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
                 35                  40                  45

Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
                 50                  55                  60

Glu Asn Gly Ile Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu
                 65                  70                  75

Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
                 80                  85                  90

Leu Pro Ser Gly Val Phe Gln Pro Leu Ala Asn Leu Ser Asn Leu
                 95                 100                 105

Asp Leu Thr Ala Asn Arg Leu His Glu Ile Thr Asn Glu Thr Phe
                110                 115                 120

Arg Gly Leu Arg Arg Leu Glu Arg Leu Tyr Leu Gly Lys Asn Arg
                125                 130                 135

Ile Arg His Ile Gln Pro Gly Ala Phe Asp Thr Leu Asp Arg Leu
                140                 145                 150

Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu Arg Ala Leu Pro Pro
                155                 160                 165

Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu Ser His Asn Ser
                170                 175                 180

Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu
                185                 190                 195

Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly
                200                 205                 210

Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp
                215                 220                 225

Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly
                230                 235                 240

Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu
                245                 250                 255

Arg Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp
```

58

Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly
275   280   285

Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe
290   295   300

Asn Cys Val Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu
305   310   315

Ser His Val Thr Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe
320   325   330

Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala
335   340   345

Asp Phe Gly Cys Pro Ala Thr Thr Thr Ala Thr Val Pro Thr
350   355   360

Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu
365   370   375

Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro
380   385   390

Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln
395   400   405

Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys
410   415   420

His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly
425   430   435

Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg
440   445   450

Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr
455   460   465

Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu
470   475   480

Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg
485   490   495

Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr
500   505   510

Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu
515   520   525

Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro
530   535   540

Gly Arg Val Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr
545   550   555

59

```
Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg
            560             565                 570

Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val
            575             580                 585

Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg
            590             595                 600

Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val
            605             610                 615

Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro
            620             625                 630

Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu
            635             640                 645

Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly
            650             655                 660

Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile
            665             670

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
 tcttcagccg cttgcgcaac ctc 23

<210> 54
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 54
 ttgctcacat ccagctcctg cagg 24

<210> 55
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 55
 tggatgttgt ccagacaacc agctggagct gtatccgagg c 41

<210> 56
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60

<400> 56
gaatcatcca cgcacctgca gctctgctga gagagtgcaa gccgtggggg 50

ttttgagctc atcttcatca ttcatatgag gaaataagtg gtaaaatcct 100

tggaaataca atgagactca tcagaaacat ttacatattt tgtagtattg 150

ttatgacagc agagggtgat gctccagagc tgccagaaga aagggaactg 200

atgaccaact gctccaacat gtctctaaga aaggttcccg cagacttgac 250

cccagccaca acgacactgg atttatccta taacctcctt tttcaactcc 300

agagttcaga ttttcattct gtctccaaac tgagagtttt gattctatgc 350

cataacagaa ttcaacagct ggatctcaaa acctttgaat tcaacaagga 400

gttaagatat ttagatttgt ctaataacag actgaagagt gtaacttggt 450

atttactggc aggtctcagg tatttagatc tttcttttaa tgactttgac 500

accatgccta tctgtgagga agctggcaac atgtcacacc tggaaatcct 550

aggtttgagt ggggcaaaaa tacaaaaatc agatttccag aaaattgctc 600

atctgcatct aaatactgtc ttcttaggat tcagaactct tcctcattat 650

gaagaaggta gcctgcccat cttaaacaca acaaaactgc acattgtttt 700

accaatggac acaaatttct gggttctttt gcgtgatgga atcaagactt 750

caaaaatatt agaaatgaca aatatagatg gcaaaagcca atttgtaagt 800

tatgaaatgc aacgaaatct tagtttagaa aatgctaaga catcggttct 850

attgcttaat aaagttgatt tactctggga cgacttttc cttatcttac 900

aatttgtttg gcatacatca gtggaacact ttcagatccg aaatgtgact 950

tttggtggta aggcttatct tgaccacaat tcatttgact actcaaatac 1000

tgtaatgaga actataaaat tggagcatgt acatttcaga gtgttttaca 1050

ttcaacagga taaaatctat ttgctttтga ccaaaatgga catagaaaac 1100

ctgacaatat caaatgcaca aatgccacac atgcttttcc cgaattatcc 1150

tacgaaattc caatatttaa attttgccaa taatatctta acagacgagt 1200

tgtttaaaag aactatccaa ctgcctcact tgaaaactct cattttgaat 1250

ggcaataaac tggagacact ttctttagta agttgctttg ctaacaacac 1300

acccttggaa cacttggatc tgagtcaaaa tctattacaa cataaaaatg 1350

atgaaaattg ctcatggcca gaaactgtgg tcaatatgaa tctgtcatac 1400

aataaattgt ctgattctgt cttcaggtgc ttgcccaaaa gtattcaaat 1450

acttgaccta aataataacc aaatccaaac tgtacctaaa gagactattc 1500

atctgatggc cttacgagaa ctaaatattg catttaattt tctaactgat 1550

ctccctggat gcagtcattt cagtagactt tcagttctga acattgaaat 1600

gaacttcatt ctcagcccat ctctggattt tgttcagagc tgccaggaag 1650

ttaaaactct aaatgcggga agaaatccat tccggtgtac ctgtgaatta 1700

aaaaatttca ttcagcttga aacatattca gaggtcatga tggttggatg 1750

gtcagattca tacacctgtg aatacccttt aaacctaagg ggaactaggt 1800

taaaagacgt tcatctccac gaattatctt gcaacacagc tctgttgatt 1850

gtcaccattg tggttattat gctagttctg gggttggctg tggccttctg 1900

ctgtctccac tttgatctgc cctggtatct caggatgcta ggtcaatgca 1950

cacaaacatg gcacagggtt aggaaaacaa cccaagaaca actcaagaga 2000

aatgtccgat tccacgcatt tatttcatac agtgaacatg attctctgtg 2050

ggtgaagaat gaattgatcc ccaatctaga gaaggaagat ggttctatct 2100

tgatttgcct ttatgaaagc tactttgacc ctggcaaaag cattagtgaa 2150

aatattgtaa gcttcattga gaaaagctat aagtccatct ttgttttgtc 2200

tcccaacttt gtccagaatg agtggtgcca ttatgaattc tactttgccc 2250

accacaatct cttccatgaa aattctgatc atataattct tatcttactg 2300

gaacccattc cattctattg cattcccacc aggtatcata aactgaaagc 2350

tctcctggaa aaaaagcat acttggaatg gcccaaggat aggcgtaaat 2400

gtgggctttt ctgggcaaac cttcgagctg ctattaatgt taatgtatta 2450

gccaccagag aaatgtatga actgcagaca ttcacagagt aaatgaaga 2500

gtctcgaggt tctacaatct ctctgatgag aacagattgt ctataaaatc 2550

ccacagtcct tgggaagttg gggaccacat acactgttgg gatgtacatt 2600

gatacaacct ttatgatggc aatttgacaa tatttattaa aataaaaaat 2650

ggttattccc ttcatatcag tttctagaag gatttctaag aatgtatcct 2700

atagaaacac cttcacaagt ttataagggc ttatggaaaa aggtgttcat 2750

cccaggattg tttataatca tgaaaaatgt ggccaggtgc agtggctcac 2800

62

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tcttgtaatc ccagcactat gggaggccaa ggtgggtgac ccacgaggtc 2850

aagagatgga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 2900

aaatacaaaa attagctggg cgtgatggtg cacgcctgta gtcccagcta 2950

cttgggaggc tgaggcagga gaatcgcttg aacccgggag gtggcagttg 3000

cagtgagctg agatcgagcc actgcactcc agcctggtga cagagcgaga 3050

ctccatctca aaaaaagaa aaaaaaaaa gaaaaaatg gaaacatcc 3100

tcatggccac aaaataaggt ctaattcaat aaattatagt acattaatgt 3150

aatataatat tacatgccac taaaaagaat aaggtagctg tatatttcct 3200

ggtatggaaa aaacatatta atatgttata aactattagg ttggtgcaaa 3250

actaattgtg gtttttgcca ttgaaatggc attgaaataa aagtgtaaag 3300

aaatctatac cagatgtagt aacagtggtt tgggtctggg aggttggatt 3350

acagggagca tttgatttct atgttgtgta tttctataat gtttgaattg 3400

tttagaatga atctgtattt cttttataag tagaaaaaaa ataaagatag 3450

tttttacagc ct 3462
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<210> 57
<211> 811
<212> PRT
<213> Homo sapiens

<400> 57
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Met Arg Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met
 1               5                  10                  15

Thr Ala Glu Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu
                20                  25                  30

Met Thr Asn Cys Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp
                35                  40                  45

Leu Thr Pro Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu
                50                  55                  60

Phe Gln Leu Gln Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg
                65                  70                  75

Val Leu Ile Leu Cys His Asn Arg Ile Gln Gln Leu Asp Leu Lys
                80                  85                  90

Thr Phe Glu Phe Asn Lys Glu Leu Arg Tyr Leu Asp Leu Ser Asn
                95                 100                 105

Asn Arg Leu Lys Ser Val Thr Trp Tyr Leu Leu Ala Gly Leu Arg
                110                115                 120
```

63

```
Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp Thr Met Pro Ile Cys
                  125                 130                 135

Glu Glu Ala Gly Asn Met Ser His Leu Glu Ile Leu Gly Leu Ser
                  140                 145                 150

Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln Lys Ile Ala His Leu
                  155                 160                 165

His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr Leu Pro His Tyr
                  170                 175                 180

Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys Leu His Ile
                  185                 190                 195

Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg Asp Gly
                  200                 205                 210

Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly Lys
                  215                 220                 225

Ser Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu
                  230                 235                 240

Asn Ala Lys Thr Ser Val Leu Leu Leu Asn Lys Val Asp Leu Leu
                  245                 250                 255

Trp Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser
                  260                 265                 270

Val Glu His Phe Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala
                  275                 280                 285

Tyr Leu Asp His Asn Ser Phe Asp Tyr Ser Asn Thr Val Met Arg
                  290                 295                 300

Thr Ile Lys Leu Glu His Val His Phe Arg Val Phe Tyr Ile Gln
                  305                 310                 315

Gln Asp Lys Ile Tyr Leu Leu Leu Thr Lys Met Asp Ile Glu Asn
                  320                 325                 330

Leu Thr Ile Ser Asn Ala Gln Met Pro His Met Leu Phe Pro Asn
                  335                 340                 345

Tyr Pro Thr Lys Phe Gln Tyr Leu Asn Phe Ala Asn Asn Ile Leu
                  350                 355                 360

Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln Leu Pro His Leu Lys
                  365                 370                 375

Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr Leu Ser Leu Val
                  380                 385                 390

Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu Asp Leu Ser
                  395                 400                 405

Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser Trp Pro
```

```
                410                        415                        420
Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser Asp
                425                        430                        435

Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu
                440                        445                        450

Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu
                455                        460                        465

Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp
                470                        475                        480

Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile
                485                        490                        495

Glu Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser
                500                        505                        510

Cys Gln Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg
                515                        520                        525

Cys Thr Cys Glu Leu Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser
                530                        535                        540

Glu Val Met Met Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr
                545                        550                        555

Pro Leu Asn Leu Arg Gly Thr Arg Leu Lys Asp Val His Leu His
                560                        565                        570

Glu Leu Ser Cys Asn Thr Ala Leu Leu Ile Val Thr Ile Val Val
                575                        580                        585

Ile Met Leu Val Leu Gly Leu Ala Val Ala Phe Cys Cys Leu His
                590                        595                        600

Phe Asp Leu Pro Trp Tyr Leu Arg Met Leu Gly Gln Cys Thr Gln
                605                        610                        615

Thr Trp His Arg Val Arg Lys Thr Thr Gln Glu Gln Leu Lys Arg
                620                        625                        630

Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser
                635                        640                        645

Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp
                650                        655                        660

Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly
                665                        670                        675

Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser Tyr
                680                        685                        690

Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp
                695                        700                        705
```

65

Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu
             710   715   720

Asn Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe
                725   730   735

Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu
                740   745   750

Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly
                755   760   765

Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu
                770   775   780

Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn
                785   790   795

Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp Cys
                800   805   810

Leu

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 58
 tcccaccagg tatcataaac tgaa   24

<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
 ttatagacaa tctgttctca tcagaga   27

<210> 60
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 60
 aaaaagcata cttggaatgg cccaaggata ggtgtaaatg   40

<210> 61

66

<400> 61

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ggggctttc ttgggcttgg ctgcttggaa cacctgcctc caaggaccgg 50

cctcggaggg gtcgccggga aagggaggga agaaggaagg gcggggccgg 100

ccccctgcg cccgccccgc gcctctgcgc gccctgtcc gccccggccc 150

agcccagccc agccccgcgg gccggtcaca cgcgcagcca gccggccgcc 200

tcccgcgccc aagcgcgccg ctctgctgtg ccctgcgccc ttgccccgcg 250

ccagcttctg cgcccgcagc ccgcccggcg ccccggtga ccgtgaccct 300

gccctgggcg cggggcggag caggcatgtc ccgcccgggg accgctaccc 350

cagcgctggc cctggtgctc ctggcagtga ccctggccgg ggtcggagcc 400

cagggcgcag ccctcgagga ccctgattat tacgggcagg agatctggag 450

ccgggagccc tactacgcgc gccggagcc cgagctcgag accttctctc 500

cgccgctgcc tgcggggccc ggggaggagt gggagcggcg cccgcaggag 550

cccaggccgc ccaagagggc caccaagccc aagaaagctc ccaagaggga 600

gaagtcggct ccggagccgc ctccaccagg taaacacagc aacaaaaaag 650

ttatgagaac caagagctct gagaaggctg ccaacgatga tcacagtgtc 700

cgtgtggccc gtgaagatgt cagagagagt tgcccacctc ttggtctgga 750

aaccttaaaa atcacagact tccagctcca tgcctccacg gtgaagcgct 800

atggcctggg ggcacatcga gggagactca catccaggc gggcattaat 850

gaaaatgatt tttatgacgg agcgtggtgc gcgggaagaa atgacctcca 900

gcagtggatt gaagtggatg ctcggcgcct gaccagattc actggtgtca 950

tcactcaagg gaggaactcc ctctggctga gtgactgggt gacatcctat 1000

aaggtcatgg tgagcaatga cagccacacg tgggtcactg ttaagaatgg 1050

atctggagac atgatatttg agggaaacag tgagaaggag atccctgttc 1100

tcaatgagct acccgtcccc atggtggccc gctacatccg cataaaccct 1150

cagtcctggt ttgataatgg gagcatctgc atgagaatgg agatcctggg 1200

ctgcccactg ccagatccta ataattatta tcaccgccgg aacgagatga 1250

ccaccactga tgacctggat tttaagcacc acaattataa ggaaatgcgc 1300

cagttgatga aagttgtgaa tgaaatgtgt cccaatatca ccagaattta 1350
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67

caacattgga aaaagccacc agggcctgaa gctgtatgct gtggagatct 1400

cagatcaccc tggggagcat gaagtcggtg agcccgagtt ccactacatc 1450

gcggggggccc acggcaatga ggtgctgggc cgggagctgc tgctgctgct 1500

ggtgcagttc gtgtgtcagg agtacttggc ccggaatgcg cgcatcgtcc 1550

acctggtgga ggagacgcgg attcacgtcc tccctccct caaccccgat 1600

ggctacgaga aggcctacga aggggggctcg gagctgggag gctggtccct 1650

gggacgctgg acccacgatg gaattgacat caacaacaac tttcctgatt 1700

taaacacgct gctctgggag gcagaggatc gacagaatgt ccccaggaaa 1750

gttcccaatc actatattgc aatccctgag tggtttctgt cggaaaatgc 1800

cacggtggct gccgagacca gagcagtcat agcctggatg gaaaaaatcc 1850

cttttgtgct gggcggcaac ctgcagggcg gcgagctggt ggtggcgtat 1900

ccctacgacc tggtgcggtc cccctggaag acgcaggaac acacccccac 1950

ccccgatgac cacgtgttcc gctggctggc ctactcctat gcctccacac 2000

accgcctcat gacagacgcc cggaggaggg tgtgccacac ggaggacttc 2050

cagaaggagg agggcactgt caatggggcc tcctggcaca ccgtcgctgg 2100

aagtctgaac gatttcagct accttcatac aaactgcttc gaactgtcca 2150

tctacgtggg ctgtgataaa tacccacatg agagccagct gcccgaggag 2200

tgggagaata accgggaatc tctgatcgtg ttcatggagc aggttcatcg 2250

tggcattaaa ggcttggtga gagattcaca tggaaaagga atcccaaacg 2300

ccattatctc cgtagaaggc attaaccatg acatccgaac agccaacgat 2350

ggggattact ggcgcctcct gaaccctgga gagtatgtgg tcacagcaaa 2400

ggccgaaggt ttcactgcat ccaccaagaa ctgtatggtt ggctatgaca 2450

tggggggccac aaggtgtgac ttcacactta gcaaaaccaa catggccagg 2500

atccgagaga tcatggagaa gtttgggaag cagcccgtca gcctgccagc 2550

caggcggctg aagctgcggg ggcggaagag acgacagcgt gggtgaccct 2600

cctgggccct tgagactcgt ctgggaccca tgcaaattaa accaacctgg 2650

tagtagctcc atagtggact cactcactgt tgtttcctct gtaattcaag 2700

aagtgcctgg aagagagggt gcattgtgag gcaggtccca aaagggaagg 2750

ctggaggctg aggctgtttt cttttctttg ttcccattta tccaaataac 2800

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ttggacagag cagcagagaa aagctgatgg gagtgagaga actcagcaag 2850

ccaacctggg aatcagagag agaaggagaa ggaggggagc ctgtccgttc 2900

agagcctctg gctgcataga aaaggattct ggtgcttccc ctgtttgcgt 2950

ggcagcaagg gttccacgtg catttgcaat ttgcacagct aaaattgcag 3000

catttcccca gctgggctgt cccaaatgtt accatttgag atgctcccag 3050

gcgtcctaag agaatccacc ctctctggcc ctgggacatt gcaagctgct 3100

acaaataaat tctgtgttct tttgacaata gcgtcattgc caagtgcaca 3150

tcagtgagcc tcttgaatct gtttagtctc cttttcaac aaaggagtgt 3200

gttcagaaaa ggagagagag gctgagatca ttcaggagtt tgttgggcag 3250

caagcatgga gcttcttgca caaattctgg gtccataaac aacccccaaa 3300

gtccctgctg atccagtagc cctggaggtt ccccaggtag ggagagccag 3350

aggtgccagc cttcctgaag ggccagaaaa tttagcctgg atctcctctt 3400

ttacctgcta ggactggaaa gagccagaag tggggtggcc tgaagccctc 3450

tctctgcttg aggtattgcc cctgtgtgga attgagtgct catgggttgg 3500

cctcatatca gcctgggagt tatttttgat atgtagaatg ccagatcttc 3550

cagattaggc taaatgtaat gaaaacctct taggattatc tgtggagcat 3600

cagtttggga agaattattg aattatcttg caagaaaaaa gtatgtctca 3650

cttttttgtta atgttgctgc ctcattgacc tgggaaaaat gaaaaaaaaa 3700

aataaagcaa atggtaagac ccttaaaaaa aaaaaaaaaa aaaaaaaaaa 3750

aaaaaaaaaa aaaaaaaaaa aa 3772
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<210> 62
<211> 756
<212> PRT
<213> Homo sapiens

<400> 62
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Met Ser Arg Pro Gly Thr Ala Thr Pro Ala Leu Ala Leu Val Leu
1               5                   10                  15

Leu Ala Val Thr Leu Ala Gly Val Gly Ala Gln Gly Ala Ala Leu
                20                  25                  30

Glu Asp Pro Asp Tyr Tyr Gly Gln Glu Ile Trp Ser Arg Glu Pro
                35                  40                  45

Tyr Tyr Ala Arg Pro Glu Pro Glu Leu Glu Thr Phe Ser Pro Pro
                50                  55                  60
```

69

```
Leu Pro Ala Gly Pro Gly Glu Glu Trp Glu Arg Arg Pro Gln Glu
                65                  70                      75

Pro Arg Pro Pro Lys Arg Ala Thr Lys Pro Lys Lys Ala Pro Lys
                80                  85                      90

Arg Glu Lys Ser Ala Pro Glu Pro Pro Pro Gly Lys His Ser
                95                 100                     105

Asn Lys Lys Val Met Arg Thr Lys Ser Ser Glu Lys Ala Ala Asn
               110                 115                     120

Asp Asp His Ser Val Arg Val Ala Arg Glu Asp Val Arg Glu Ser
               125                 130                     135

Cys Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln
               140                 145                     150

Leu His Ala Ser Thr Val Lys Arg Tyr Gly Leu Gly Ala His Arg
               155                 160                     165

Gly Arg Leu Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr
               170                 175                     180

Asp Gly Ala Trp Cys Ala Gly Arg Asn Asp Leu Gln Gln Trp Ile
               185                 190                     195

Glu Val Asp Ala Arg Arg Leu Thr Arg Phe Thr Gly Val Ile Thr
               200                 205                     210

Gln Gly Arg Asn Ser Leu Trp Leu Ser Asp Trp Val Thr Ser Tyr
               215                 220                     225

Lys Val Met Val Ser Asn Asp Ser His Thr Trp Val Thr Val Lys
               230                 235                     240

Asn Gly Ser Gly Asp Met Ile Phe Glu Gly Asn Ser Glu Lys Glu
               245                 250                     255

Ile Pro Val Leu Asn Glu Leu Pro Val Pro Met Val Ala Arg Tyr
               260                 265                     270

Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp Asn Gly Ser Ile Cys
               275                 280                     285

Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro Asp Pro Asn Asn
               290                 295                     300

Tyr Tyr His Arg Arg Asn Glu Met Thr Thr Thr Asp Asp Leu Asp
               305                 310                     315

Phe Lys His His Asn Tyr Lys Glu Met Arg Gln Leu Met Lys Val
               320                 325                     330

Val Asn Glu Met Cys Pro Asn Ile Thr Arg Ile Tyr Asn Ile Gly
               335                 340                     345

Lys Ser His Gln Gly Leu Lys Leu Tyr Ala Val Glu Ile Ser Asp
```

70

His Pro Gly Glu His Glu Val Gly Glu Pro Glu Phe His Tyr Ile
                365   370   375

Ala Gly Ala His Gly Asn Glu Val Leu Gly Arg Glu Leu Leu Leu
                380   385   390

Leu Leu Val Gln Phe Val Cys Gln Glu Tyr Leu Ala Arg Asn Ala
                395   400   405

Arg Ile Val His Leu Val Glu Glu Thr Arg Ile His Val Leu Pro
                410   415   420

Ser Leu Asn Pro Asp Gly Tyr Glu Lys Ala Tyr Glu Gly Gly Ser
                425   430   435

Glu Leu Gly Gly Trp Ser Leu Gly Arg Trp Thr His Asp Gly Ile
                440   445   450

Asp Ile Asn Asn Asn Phe Pro Asp Leu Asn Thr Leu Leu Trp Glu
                455   460   465

Ala Glu Asp Arg Gln Asn Val Pro Arg Lys Val Pro Asn His Tyr
                470   475   480

Ile Ala Ile Pro Glu Trp Phe Leu Ser Glu Asn Ala Thr Val Ala
                485   490   495

Ala Glu Thr Arg Ala Val Ile Ala Trp Met Glu Lys Ile Pro Phe
                500   505   510

Val Leu Gly Gly Asn Leu Gln Gly Gly Glu Leu Val Val Ala Tyr
                515   520   525

Pro Tyr Asp Leu Val Arg Ser Pro Trp Lys Thr Gln Glu His Thr
                530   535   540

Pro Thr Pro Asp Asp His Val Phe Arg Trp Leu Ala Tyr Ser Tyr
                545   550   555

Ala Ser Thr His Arg Leu Met Thr Asp Ala Arg Arg Arg Val Cys
                560   565   570

His Thr Glu Asp Phe Gln Lys Glu Glu Gly Thr Val Asn Gly Ala
                575   580   585

Ser Trp His Thr Val Ala Gly Ser Leu Asn Asp Phe Ser Tyr Leu
                590   595   600

His Thr Asn Cys Phe Glu Leu Ser Ile Tyr Val Gly Cys Asp Lys
                605   610   615

Tyr Pro His Glu Ser Gln Leu Pro Glu Glu Trp Glu Asn Asn Arg
                620   625   630

Glu Ser Leu Ile Val Phe Met Glu Gln Val His Arg Gly Ile Lys
                635   640   645

```
Gly Leu Val Arg Asp Ser His Gly Lys Gly Ile Pro Asn Ala Ile
              650                 655                 660

Ile Ser Val Glu Gly Ile Asn His Asp Ile Arg Thr Ala Asn Asp
              665                 670                 675

Gly Asp Tyr Trp Arg Leu Leu Asn Pro Gly Glu Tyr Val Val Thr
              680                 685                 690

Ala Lys Ala Glu Gly Phe Thr Ala Ser Thr Lys Asn Cys Met Val
              695                 700                 705

Gly Tyr Asp Met Gly Ala Thr Arg Cys Asp Phe Thr Leu Ser Lys
              710                 715                 720

Thr Asn Met Ala Arg Ile Arg Glu Ile Met Glu Lys Phe Gly Lys
              725                 730                 735

Gln Pro Val Ser Leu Pro Ala Arg Arg Leu Lys Leu Arg Gly Arg
              740                 745                 750

Lys Arg Arg Gln Arg Gly
              755
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<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 63
 gttctcaatg agctacccgt cccc 24

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 64
 cgcgatgtag tggaactcgg gctc 24

<210> 65
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
 atccgcataa accctcagtc ctggtttgat aatgggagca tctgcatgag 50

<210> 66

72

<211> 2854
<212> DNA
<213> Homo sapiens

<400> 66
ctaagaggac aagatgaggc ccggcctctc atttctccta gcccttctgt 50

tcttccttgg ccaagctgca ggggatttgg gggatgtggg acctccaatt 100

cccagccccg gcttcagctc tttcccaggt gttgactcca gctccagctt 150

cagctccagc tccaggtcgg gctccagctc cagccgcagc ttaggcagcg 200

gaggttctgt gtcccagttg ttttccaatt tcaccggctc cgtggatgac 250

cgtgggacct gccagtgctc tgtttccctg ccagacacca cctttcccgt 300

ggacagagtg gaacgcttgg aattcacagc tcatgttctt tctcagaagt 350

ttgagaaaga actttctaaa gtgagggaat atgtccaatt aattagtgtg 400

tatgaaaaga aactgttaaa cctaactgtc cgaattgaca tcatggagaa 450

ggataccatt tcttacactg aactggactt cgagctgatc aaggtagaag 500

tgaaggagat ggaaaaactg gtcatacagc tgaaggagag ttttggtgga 550

agctcagaaa ttgttgacca gctggaggtg gagataagaa atatgactct 600

cttggtagag aagcttgaga cactagacaa aaacaatgtc cttgccattc 650

gccgagaaat cgtggctctg aagaccaagc tgaaagagtg tgaggcctct 700

aaagatcaaa acacccctgt cgtccaccct cctcccactc cagggagctg 750

tggtcatggt ggtgtggtga acatcagcaa accgtctgtg gttcagctca 800

actggagagg gttttcttat ctatatggtg cttggggtag ggattactct 850

ccccagcatc caaacaaagg actgtattgg gtggcgccat gaatacaga 900

tgggagactg ttggagtatt atagactgta caacacactg gatgatttgc 950

tattgtatat aaatgctcga gagttgcgga tcacctatgg ccaaggtagt 1000

ggtacagcag tttacaacaa caacatgtac gtcaacatgt acaacaccgg 1050

gaatattgcc agagttaacc tgaccaccaa cacgattgct gtgactcaaa 1100

ctctccctaa tgctgcctat aataaccgct tttcatatgc taatgttgct 1150

tggcaagata ttgactttgc tgtggatgag aatggattgt gggttatttta 1200

ttcaactgaa gccagcactg gtaacatggt gattagtaaa ctcaatgaca 1250

ccacacttca ggtgctaaac acttggtata ccaagcagta taaaccatct 1300

gcttctaacg ccttcatggt atgtgggggtt ctgtatgcca cccgtactat 1350

73

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gaacaccaga  acagaagaga  tttttacta  ttatgacaca  aacacaggga  1400

aagagggcaa  actagacatt  gtaatgcata  agatgcagga  aaaagtgcag  1450

agcattaact  ataacccttt  tgaccagaaa  ctttatgtct  ataacgatgg  1500

ttaccttctg  aattatgatc  tttctgtctt  gcagaagccc  cagtaagctg  1550

tttaggagtt  agggtgaaag  agaaaatgtt  tgttgaaaaa  atagtcttct  1600

ccacttactt  agatatctgc  aggggtgtct  aaaagtgtgt  tcattttgca  1650

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gggcctagtg  aagcctactg  tgaggaggct  tcactagaag  ccttaaatta  1850

ggaattaagg  aacttaaaac  tcagtatggc  gtctagggat  tctttgtaca  1900

ggaaatattg  cccaatgact  agtcctcatc  catgtagcac  cactaattct  1950

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agctcctcga  gggaccaaat  ctccaacttt  tttttcccct  cactagcacc  2050

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attctacatc  tgtaaagtgc  tgagtttтat  ggagagaggc  ctttttatgc  2150

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cctgcttttt  cttttctctc  attgtccacc  ttactaaaag  tcagtagaat  2250

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acttactaac  caattccacc  ccccaccaac  ccccttctac  tgcctacttt  2350

aaaaaaatta  atagttttct  atggaactga  tctaagatta  gaaaaattaa  2400

ttttctttaa  tttcattatg  gacttttatt  tacatgactc  taagactata  2450

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cttttgaatg  actttatcat  ctagtctttg  tctatttttc  ctttgatgtt  2750

caagtcctag  tctataggat  tggcagttta  aatgctttac  tccccctttt  2800
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74

aaaataaatg attaaaatgt gctttgaaaa aaaaaaaaaa aaaaaaaaaa 2850

aaaa 2854

<210> 67
<211> 510
<212> PRT
<213> Homo sapiens

<400> 67
Met Arg Pro Gly Leu Ser Phe Leu Leu Ala Leu Leu Phe Phe Leu
 1   5   10   15

Gly Gln Ala Ala Gly Asp Leu Gly Asp Val Gly Pro Pro Ile Pro
                20   25   30

Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser
                35   40   45

Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser Arg Ser Leu
                50   55   60

Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly
                65   70   75

Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu Pro
                80   85   90

Asp Thr Thr Phe Pro Val Asp Arg Val Glu Arg Leu Glu Phe Thr
                95   100   105

Ala His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val
                110   115   120

Arg Glu Tyr Val Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu
                125   130   135

Asn Leu Thr Val Arg Ile Asp Ile Met Glu Lys Asp Thr Ile Ser
                140   145   150

Tyr Thr Glu Leu Asp Phe Glu Leu Ile Lys Val Glu Val Lys Glu
                155   160   165

Met Glu Lys Leu Val Ile Gln Leu Lys Glu Ser Phe Gly Gly Ser
                170   175   180

Ser Glu Ile Val Asp Gln Leu Glu Val Glu Ile Arg Asn Met Thr
                185   190   195

Leu Leu Val Glu Lys Leu Glu Thr Leu Asp Lys Asn Asn Val Leu
                200   205   210

Ala Ile Arg Arg Glu Ile Val Ala Leu Lys Thr Lys Leu Lys Glu
                215   220   225

Cys Glu Ala Ser Lys Asp Gln Asn Thr Pro Val Val His Pro Pro
                230   235   240

75

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Pro Thr Pro Gly Ser Cys Gly His Gly Gly Val Val Asn Ile Ser
            245             250                     255

Lys Pro Ser Val Val Gln Leu Asn Trp Arg Gly Phe Ser Tyr Leu
            260             265                     270

Tyr Gly Ala Trp Gly Arg Asp Tyr Ser Pro Gln His Pro Asn Lys
            275             280                     285

Gly Leu Tyr Trp Val Ala Pro Leu Asn Thr Asp Gly Arg Leu Leu
            290             295                     300

Glu Tyr Tyr Arg Leu Tyr Asn Thr Leu Asp Asp Leu Leu Leu Tyr
            305             310                     315

Ile Asn Ala Arg Glu Leu Arg Ile Thr Tyr Gly Gln Gly Ser Gly
            320             325                     330

Thr Ala Val Tyr Asn Asn Asn Met Tyr Val Asn Met Tyr Asn Thr
            335             340                     345

Gly Asn Ile Ala Arg Val Asn Leu Thr Thr Asn Thr Ile Ala Val
            350             355                     360

Thr Gln Thr Leu Pro Asn Ala Ala Tyr Asn Asn Arg Phe Ser Tyr
            365             370                     375

Ala Asn Val Ala Trp Gln Asp Ile Asp Phe Ala Val Asp Glu Asn
            380             385                     390

Gly Leu Trp Val Ile Tyr Ser Thr Glu Ala Ser Thr Gly Asn Met
            395             400                     405

Val Ile Ser Lys Leu Asn Asp Thr Thr Leu Gln Val Leu Asn Thr
            410             415                     420

Trp Tyr Thr Lys Gln Tyr Lys Pro Ser Ala Ser Asn Ala Phe Met
            425             430                     435

Val Cys Gly Val Leu Tyr Ala Thr Arg Thr Met Asn Thr Arg Thr
            440             445                     450

Glu Glu Ile Phe Tyr Tyr Tyr Asp Thr Asn Thr Gly Lys Glu Gly
            455             460                     465

Lys Leu Asp Ile Val Met His Lys Met Gln Glu Lys Val Gln Ser
            470             475                     480

Ile Asn Tyr Asn Pro Phe Asp Gln Lys Leu Tyr Val Tyr Asn Asp
            485             490                     495

Gly Tyr Leu Leu Asn Tyr Asp Leu Ser Val Leu Gln Lys Pro Gln
            500             505                     510
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<210> 68
<211> 410
<212> DNA
<213> Homo sapiens

76

<220>
<221> unsure
<222> 206, 217, 387
<223> unknown base

<400> 68
gctctgaaga ccaagctgaa agagtgtgag gcctctaaag atcaaacacc 50

cctgtcgtcc accctcctcc cactccaggg agctgtggtc atggtggtgt 100

ggtgaacatc agcaaaccgt ctgtggttca gctcaactgg agagggtttt 150

cttatctata tggtgcttgg ggtagggatt actctcccca gcatccaaac 200

aaaggnatgt attgggnggc gccattgaat acagatggga gactgttgga 250

gtattataga ctgtacaacc cactggatga tttgctattg tatataaatg 300

ctcgagagtt gcggatcacc tatggccaag gtagtggtac agcagtttac 350

aacaacaaca tgtacgtcaa catgtacaac accgggnata ttgccagagt 400

taacctgacc 410

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
agctgtggtc atggtggtgt ggtg 24

<210> 70
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ctaccttggc cataggtgat ccgc 24

<210> 71
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
catcagcaaa ccgtctgtgg ttcagctcaa ctggagaggg tt 42

<210> 72

77

<211> 3127
<212> DNA
<213> Homo sapiens

<400> 72
tctcgcagat agtaaataat ctcggaaagg cgagaaagaa gctgtctcca 50

tcttgtctgt atccgctgct cttgtgacgt tgtggagatg gggagcgtcc 100

tggggctgtg ctccatggcg agctggatac catgtttgtg tggaagtgcc 150

ccgtgtttgc tatgccgatg ctgtcctagt ggaaacaact ccactgtaac 200

tagattgatc tatgcacttt tcttgcttgt tggagtatgt gtagcttgtg 250

taatgttgat accaggaatg gaagaacaac tgaataagat tcctggattt 300

tgtgagaatg agaaaggtgt tgtcccttgt aacattttgg ttggctataa 350

agctgtatat cgtttgtgct ttggtttggc tatgttctat cttcttctct 400

ctttactaat gatcaaagtg aagagtagca gtgatcctag agctgcagtg 450

cacaatggat tttggttctt taaatttgct gcagcaattg caattattat 500

tggggcattc ttcattccag aaggaacttt tacaactgtg tggttttatg 550

taggcatggc aggtgccttt tgtttcatcc tcatacaact agtcttactt 600

attgattttg cacattcatg gaatgaatcg tgggttgaaa aaatggaaga 650

agggaactcg agatgttggt atgcagcctt gttatcagct acagctctga 700

attatctgct gtctttagtt gctatcgtcc tgttctttgt ctactacact 750

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cctctgcgtt ggtgcttctg taatgtctat actgccaaaa atccaagaat 850

cacaaccaag atctggtttg ttacagtctt cagtaattac agtctacaca 900

atgtatttga catggtcagc tatgaccaat gaaccagaaa caaattgcaa 950

cccaagtcta ctaagcataa ttggctacaa tacaacaagc actgtcccaa 1000

aggaagggca gtcagtccag tggtggcatg ctcaaggaat tataggacta 1050

attctctttt tgttgtgtgt attttattcc agcatccgta cttcaaacaa 1100

tagtcaggtt aataaactga ctctaacaag tgatgaatct acattaatag 1150

aagatggtgg agctagaagt gatggatcac tggaggatgg ggacgatgtt 1200

caccgagctg tagataatga aagggatggt gtcacttaca gttattcctt 1250

ctttcacttc atgcttttcc tggcttcact ttatatcatg atgaccctta 1300

ccaactggtc caggtatgaa ccctctcgtg agatgaaaag tcagtggaca 1350

78

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ttggacactc gtggcaccac ttgttcttac aaatcgtgat tttgactgag 1450

tgagacttct agcatgaaag tcccactttg attattgctt atttgaaaac 1500

agtattccca acttttgtaa agttgtgtat gttttttgctt cccatgtaac 1550

ttctccagtg ttctggcatg aattagattt tactgcttgt cattttgtta 1600

ttttcttacc aagtgcattg atatgtgaag tagaatgaat tgcagaggaa 1650

agttttatga atatggtgat gagttagtaa aagtggccat tattgggctt 1700

attctctgct ctatagttgt gaaatgaaga gtaaaaacaa atttgtttga 1750

ctattttaaa attatattag accttaagct gttttagcaa gcattaaagc 1800

aaatgtatgg ctgccttttg aaatatttga tgtgttgcct ggcaggatac 1850

tgcaaagaac atggtttatt ttaaaattta taaacaagtc acttaaatgc 1900

cagttgtctg aaaaatctta taaggtttta cccttgatac ggaatttaca 1950

caggtaggga gtgtttagtg gacaatagtg taggttatgg atggaggtgt 2000

cggtactaaa ttgaataacg agtaaataat cttacttggg tagagatggc 2050

ctttgccaac aaagtgaact gttttggttg ttttaaactc atgaagtatg 2100

ggttcagtgg aaatgtttgg aactctgaag gatttagaca aggttttgaa 2150

aaggataatc atgggttaga aggaagtgtt ttgaaagtca ctttgaaagt 2200

tagttttggg cccagcacgg tagctcaccc ttggtaatcc cagcactttg 2250

ggagcttaag tgggtagatt acttgagccc aggaattcag accagcttgg 2300

cacatggtga acctgttcta taaaaataat ctggctttga gcatatgcct 2350

gtggtccagc actgagaggc tagtgaagat tgctgagccc agagccaaag 2400

gttgcagtga gcaagtcacg tcactgcact ctagctggca cagagtaagc 2450

caaaaaaata tatatatatt gaaatcaagg aggcaaaatt ttgacaggga 2500

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tagtccagtt ctctcattta aaaaaatgaa gacactgaaa tacagactta 2600

aatagctcag atagctaatt aggaaatttc aagttggcca ataatagcat 2650

tctctctgac atttaaaaat aatttctatt caaaatacat gcatattgat 2700

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catgacccat aaacaggtca gaagaatgat ggaatgtttt agaataaact 2800
```

79

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cctgcttata gtatactaca cagttcaaaa gatgtttaaa atgctttgt 2850

atttactgcc atgtaattga aatatataga ttattgtaac ctttcaacct 2900

gaaaatcaag cagtatgaga gtttagttat ttgtatgtgt cactagtgtc 2950

taatgaagct tttaaaatct acaatttctt ctttaaaaat atttattaat 3000

gtgaatggaa tataacaatt cagcttaatt ccccaacctt attctgtgtg 3050

tagacattgt attccacaat tttgaatggc tgtgttttac ctctaaataa 3100

atgaattcag agaaaaaaa aaaaaaa 3127
```

<210> 73
<211> 453
<212> PRT
<213> Homo sapiens

<400> 73

```
Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro
 1               5                  10                  15

Cys Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro
                20                  25                  30

Ser Gly Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe
                35                  40                  45

Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly
                50                  55                  60

Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu
                65                  70                  75

Lys Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val
                80                  85                  90

Tyr Arg Leu Cys Phe Gly Leu Ala Met Phe Tyr Leu Leu Leu Ser
                95                  100                 105

Leu Leu Met Ile Lys Val Lys Ser Ser Ser Asp Pro Arg Ala Ala
                110                 115                 120

Val His Asn Gly Phe Trp Phe Phe Lys Phe Ala Ala Ala Ile Ala
                125                 130                 135

Ile Ile Ile Gly Ala Phe Phe Ile Pro Glu Gly Thr Phe Thr Thr
                140                 145                 150

Val Trp Phe Tyr Val Gly Met Ala Gly Ala Phe Cys Phe Ile Leu
                155                 160                 165

Ile Gln Leu Val Leu Leu Ile Asp Phe Ala His Ser Trp Asn Glu
                170                 175                 180

Ser Trp Val Glu Lys Met Glu Glu Gly Asn Ser Arg Cys Trp Tyr
                185                 190                 195
```

80

```
Ala Ala Leu Leu Ser Ala Thr Ala Leu Asn Tyr Leu Leu Ser Leu
            200                 205                 210

Val Ala Ile Val Leu Phe Phe Val Tyr Tyr Thr His Pro Ala Ser
            215                 220                 225

Cys Ser Glu Asn Lys Ala Phe Ile Ser Val Asn Met Leu Leu Cys
            230                 235                 240

Val Gly Ala Ser Val Met Ser Ile Leu Pro Lys Ile Gln Glu Ser
            245                 250                 255

Gln Pro Arg Ser Gly Leu Leu Gln Ser Ser Val Ile Thr Val Tyr
            260                 265                 270

Thr Met Tyr Leu Thr Trp Ser Ala Met Thr Asn Glu Pro Glu Thr
            275                 280                 285

Asn Cys Asn Pro Ser Leu Leu Ser Ile Ile Gly Tyr Asn Thr Thr
            290                 295                 300

Ser Thr Val Pro Lys Glu Gly Gln Ser Val Gln Trp Trp His Ala
            305                 310                 315

Gln Gly Ile Ile Gly Leu Ile Leu Phe Leu Leu Cys Val Phe Tyr
            320                 325                 330

Ser Ser Ile Arg Thr Ser Asn Asn Ser Gln Val Asn Lys Leu Thr
            335                 340                 345

Leu Thr Ser Asp Glu Ser Thr Leu Ile Glu Asp Gly Gly Ala Arg
            350                 355                 360

Ser Asp Gly Ser Leu Glu Asp Gly Asp Asp Val His Arg Ala Val
            365                 370                 375

Asp Asn Glu Arg Asp Gly Val Thr Tyr Ser Tyr Ser Phe Phe His
            380                 385                 390

Phe Met Leu Phe Leu Ala Ser Leu Tyr Ile Met Met Thr Leu Thr
            395                 400                 405

Asn Trp Ser Arg Tyr Glu Pro Ser Arg Glu Met Lys Ser Gln Trp
            410                 415                 420

Thr Ala Val Trp Val Lys Ile Ser Ser Ser Trp Ile Gly Ile Val
            425                 430                 435

Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val Leu Thr Asn Arg
            440                 445                 450

Asp Phe Asp
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<210> 74
<211> 480
<212> DNA
<213> Homo sapiens

81

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<220>
<221> unsure
<222> 48, 163
<223> unknown base

<400> 74
 gcgagaaaga agctgtctcc atcttgtctg tatcccgctg cttcttgnga 50

 cgttgtggag atggggagcg tccctggggc tgtgctccat ggcgagctgg 100

 ataccatgtt tgtgtggaag tgccccgtgt ttgctatgcc gatgctgtcc 150

 tagtggaaac aantccactg taactagatt gatctatgca cttttcttgc 200

 ttgttggagt atgtgtagct tgtgtaatgt tgataccagg aatggaagaa 250

 caactgaata agattcctgg attttgtgag aatgagaaag gtgttgtccc 300

 ttgtaacatt ttggttggct ataaagctgt atatcgtttg tgctttggtt 350

 tggctatgtt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400

 agcagtgatc ctagagctgc agtgcacaat ggattttggt tctttaaatt 450

 tgctgcagca attgcaatta ttattggggc 480

<210> 75
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323
<223> unknown base

<400> 75
 gttattgtga actttgtgga gatgggaggt cntggggctg tgttccatgg 50

 cgagctggat accangtttg tgtggaagtg ccccgtgttt gntatgccga 100

 tgctgtccta gtggaaacaa ntccactgta attagattga tntatgcact 150

 tttnttgctt gttggagtan gtgtagcttg tgtaatgttg ataccaggaa 200

 tggaagaaca actgaataag attcctggat tttgtgagaa tgagaaaggt 250

 gttgtccctt gtaacatttt ggttggctat aaagctgtat atngtttgtg 300

 ctttggtttg gctangttct atnttcttct ctctttacta atgatcaaag 350

 tgaagagtag cagtgatcct agagctgcag tgcacaatgg attttggttt 400

 tttaaatttg ctgcagcaat tgcaattatt attggggc 438

<210> 76
<211> 473
<212> DNA
```

<213> Homo sapiens

<220>
<221> unsure
<222> 48
<223> unknown base

<400> 76
 aagaagctgt ctccatcttg tctgtatccg ctgctcttgt gaacgttntg 50

 gagatgggga gcgtccttgg ggttgtgctc catggcgagc tggataccat 100

 gtttgtgtgg aagtgccccg tgtttgctat gccgatgctg tcctagtgga 150

 aacaactcca ctgtaactag attgatctat gcacttttct tgcttgttgg 200

 agtatgtgta gcttgtgtaa tgttgatacc aggaatggaa gaacaactga 250

 ataagattcc tggattttgt gagaatgaga aaggtgttgt cccttgtaac 300

 attttggttg gctataaagc tgtatatcgt ttgtgctttg gtttggctat 350

 gttctatctt cttctctctt tactaatgat caaagtgaag agtagcagtg 400

 atcctagagc tgcagtgcac aatggatttt ggttctttaa atttgctgca 450

 gcaattgcaa ttattattgg ggc 473

<210> 77
<211> 666
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 21, 111
<223> unknown base

<400> 77
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 acttttcct tgcttgttgg agtatgtgta gctttgtgta atgttgttcc 100

 caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150

 gaaaggtgtt gtccccttgt aacatttttg gttggctata aagctgtata 200

 tcgtttgtgc tttggtttgg ctatgttcta tcttcttctc tctttactaa 250

 tgatcaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300

 ttttggttct ttaaatttgc tgcagcaatt gcaattatta ttggggcatt 350

 cttcattcca gaaggaactt ttacaactgt gtggtttat gtaggcatgg 400

 caggtgcctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450

 gcacattcat ggaatgaatc gtgggttgaa aaaatggaag aagggaactc 500

```
gagatgttgg tatgcagcct tgttatcagc tacagctctg aattatctgc 550

tgtctttagt tgctatcgtc ctgttctttg tctactacac tcatccagcc 600

agttgttcag aaaacaaggc gttcatcagt gtcaacatgc tcctctgcgt 650

tggtgcttct gtaatg 666
```

<210> 78
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 78
```
 atgtttgtgt ggaagtgccc cg 22
```

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
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 gtcaacatgc tcctctgc 18
```

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
```
 aatccattgt gcactgcagc tctagg 26
```

<210> 81
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
```
 gagcatgcca ccactggact gac 23
```

<210> 82
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 82
 gccgatgctg tcctagtgga aacaactcca ctgtaactag attgatctat 50

 gcac 54

<210> 83
<211> 3906
<212> DNA
<213> Homo sapiens

<400> 83
 ctcgggcgcg cacaggcagc tcggtttgcc ctgcgattga gctgcgggtc 50

 gcggccggcg ccggcctctc caatggcaaa tgtgtgtggc tggaggcgag 100

 cgcgaggctt tcggcaaagg cagtcgagtg tttgcagacc ggggcgagtc 150

 ctgtgaaagc agataaaaga aaacatttat taacgtgtca ttacgagggg 200

 agcgcccggc cggggctgtc gcactccccg cggaacattt ggctccctcc 250

 agctccgaga gaggagaaga agaaagcgga aaagaggcag attcacgtcg 300

 tttccagcca agtggacctg atcgatggcc ctcctgaatt tatcacgata 350

 tttgatttat tagcgatgcc ccctggtttg tgtgttacgc acacacacgt 400

 gcacacaagg ctctggctcg cttccctccc tcgtttccag ctcctgggcg 450

 aatcccacat ctgtttcaac tctccgccga gggcgagcag gagcgagagt 500

 gtgtcgaatc tgcgagtgaa gagggacgag ggaaaagaaa caaagccaca 550

 gacgcaactt gagactcccg catcccaaaa gaagcaccag atcagcaaaa 600

 aaagaagatg ggcccccga gcctcgtgct gtgcttgctg tccgcaactg 650

 tgttctccct gctgggtgga agctcggcct tcctgtcgca ccaccgcctg 700

 aaaggcaggt ttcagaggga ccgcaggaac atccgcccca acatcatcct 750

 ggtgctgacg gacgaccagg atgtggagct gggttccatg caggtgatga 800

 acaagacccg gcgcatcatg gagcagggcg gggcgcactt catcaacgcc 850

 ttcgtgacca cacccatgtg ctgcccctca cgctcctcca tcctcactgg 900

 caagtacgtc cacaaccaca acacctacac caacaatgag aactgctcct 950

 cgccctcctg gcaggcacag cacgagagcc gcacctttgc cgtgtacctc 1000

 aatagcactg gctaccggac agctttcttc gggaagtatc ttaatgaata 1050

 caacggctcc tacgtgccac ccggctggaa ggagtgggtc ggactcctta 1100

 aaaactcccg cttttataac tacacgctgt gtcggaacgg ggtgaaagag 1150

aagcacggct ccgactactc caaggattac ctcacagacc tcatcaccaa 1200

tgacagcgtg agcttcttcc gcacgtccaa gaagatgtac ccgcacaggc 1250

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gagctacaac tacgcgccca acccggacaa acactggatc atgcgctaca 1400

cggggcccat gaagcccatc cacatggaat tcaccaacat gctccagcgg 1450

aagcgcttgc agaccctcat gtcggtggac gactccatgg agacgattta 1500

caacatgctg gttgagacgg gcgagctgga caacacgtac atcgtataca 1550

ccgccgacca cggttaccac atcggccagt ttggcctggt gaaagggaaa 1600

tccatgccat atgagtttga catcagggtc ccgttctacg tgaggggccc 1650

caacgtggaa gccggctgtc tgaatcccca catcgtcctc aacattgacc 1700

tggcccccac catcctggac attgcaggcc tggacatacc tgcggatatg 1750

gacgggaaat ccatcctcaa gctgctggac acggagcggc cggtgaatcg 1800

gtttcacttg aaaaagaaga tgagggtctg gcgggactcc ttcttggtgg 1850

agagaggcaa gctgctacac aagagagaca tgacaaggt ggacgcccag 1900

gaggagaact ttctgcccaa gtaccagcgt gtgaaggacc tgtgtcagcg 1950

tgctgagtac cagacggcgt gtgagcagct gggacagaag tggcagtgtg 2000

tggaggacgc cacggggaag ctgaagctgc ataagtgcaa gggccccatg 2050

cggctgggcg gcagcagagc cctctccaac ctcgtgccca agtactacgg 2100

gcagggcagc gaggcctgca cctgtgacag cgggggactac aagctcagcc 2150

tggccggacg ccggaaaaaa ctcttcaaga agaagtacaa ggccagctat 2200

gtccgcagtc gctccatccg ctcagtggcc atcgaggtgg acggcagggt 2250

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agtgacacat cggtgctaca tcctagagaa cgacacagtc cagtgtgacc 2450

tggacctgta caagtccctg caggcctgga aagaccacaa gctgcacatc 2500

gaccacgaga ttgaaaccct gcagaacaaa attaagaacc tgagggaagt 2550

ccgaggtcac ctgaagaaaa agcggccaga agaatgtgac tgtcacaaaa 2600

86

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tcagctacca cacccagcac aaaggccgcc tcaagcacag aggctccagt 2650

ctgcatcctt tcaggaaggg cctgcaagag aaggacaagg tgtggctgtt 2700

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agaacaacga cacgtgcagc atgccaggcc tcacgtgctt cacccacgac 2800

aaccagcact ggcagacggc gcctttctgg acactggggc ctttctgtgc 2850

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tgtgctattg gccaggaggc ctgagaaagc aagcacgcac tctcagtcaa 3350

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gtccattttt gccctgctt ttgctttgga ttatacctca ccagctgcac 3450

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tctcccaagg gcgaaagtca ttggaatttt taaatcatag gggaaaagca 3600

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tttgacaatg agtcagtagc acaaaagaga tgacatttac ctagcactat 3750

aaaccctggt tgcctctgaa gaaactgcct tcattgtata tatgtgacta 3800

tttacatgta atcaacatgg gaactttag gggaacctaa taagaaatcc 3850

caattttcag gagtggtggt gtcaataaac gctctgtggc cagtgtaaaa 3900

gaaaaa 3906
```

<210> 84
<211> 867
<212> PRT
<213> Homo sapiens

87

<400> 84

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Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val
 1               5                  10                  15

Phe Ser Leu Leu Gly Gly Ser Ser Ala Phe Leu Ser His His Arg
                20              25                  30

Leu Lys Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn
                35              40                  45

Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser
                50              55                  60

Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly
                65              70                  75

Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro
                80              85                  90

Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn
                95              100                 105

Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala
                110             115                 120

Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly
                125             130                 135

Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly
                140             145                 150

Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys
                155             160                 165

Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys
                170             175                 180

Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu
                185             190                 195

Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met
                200             205                 210

Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro
                215             220                 225

His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
                230             235                 240

Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn
                245             250                 255

Pro Asp Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro
                260             265                 270

Ile His Met Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln
                275             280                 285
```

88

Thr Leu Met Ser Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met
                    290   295   300

Leu Val Glu Thr Gly Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr
                    305   310   315

Ala Asp His Gly Tyr His Ile Gly Gln Phe Gly Leu Val Lys Gly
                    320   325   330

Lys Ser Met Pro Tyr Glu Phe Asp Ile Arg Val Pro Phe Tyr Val
                    335   340   345

Arg Gly Pro Asn Val Glu Ala Gly Cys Leu Asn Pro His Ile Val
                    350   355   360

Leu Asn Ile Asp Leu Ala Pro Thr Ile Leu Asp Ile Ala Gly Leu
                    365   370   375

Asp Ile Pro Ala Asp Met Asp Gly Lys Ser Ile Leu Lys Leu Leu
                    380   385   390

Asp Thr Glu Arg Pro Val Asn Arg Phe His Leu Lys Lys Lys Met
                    395   400   405

Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg Gly Lys Leu Leu
                    410   415   420

His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu Glu Asn Phe
                    425   430   435

Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg Ala Glu
                    440   445   450

Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys Val
                    455   460   465

Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro
                    470   475   480

Met Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys
                    485   490   495

Tyr Tyr Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp
                    500   505   510

Tyr Lys Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys
                    515   520   525

Lys Tyr Lys Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val
                    530   535   540

Ala Ile Glu Val Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp
                    545   550   555

Ala Ala Gln Pro Arg Asn Leu Thr Lys Arg His Trp Pro Gly Ala
                    560   565   570

Pro Glu Asp Gln Asp Asp Lys Asp Gly Gly Asp Phe Ser Gly Thr

89

```
                    575                    580                    585

Gly Gly Leu Pro Asp Tyr Ser Ala Ala Asn Pro Ile Lys Val Thr
                590                    595                    600

His Arg Cys Tyr Ile Leu Glu Asn Asp Thr Val Gln Cys Asp Leu
                605                    610                    615

Asp Leu Tyr Lys Ser Leu Gln Ala Trp Lys Asp His Lys Leu His
                620                    625                    630

Ile Asp His Glu Ile Glu Thr Leu Gln Asn Lys Ile Lys Asn Leu
                635                    640                    645

Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg Pro Glu Glu Cys
                650                    655                    660

Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys Gly Arg Leu
                665                    670                    675

Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly Leu Gln
                680                    685                    690

Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys Lys
                695                    700                    705

Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys
                710                    715                    720

Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp
                725                    730                    735

Gln Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr
                740                    745                    750

Ser Ala Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu
                755                    760                    765

Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu
                770                    775                    780

Tyr Phe Asp Leu Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val
                785                    790                    795

Asn Thr Leu Asp Arg Asp Val Leu Asn Gln Leu His Val Gln Leu
                800                    805                    810

Met Glu Leu Arg Ser Cys Lys Gly Tyr Lys Gln Cys Asn Pro Arg
                815                    820                    825

Thr Arg Asn Met Asp Leu Asp Gly Gly Ser Tyr Glu Gln Tyr Arg
                830                    835                    840

Gln Phe Gln Arg Arg Lys Trp Pro Glu Met Lys Arg Pro Ser Ser
                845                    850                    855

Lys Ser Leu Gly Gln Leu Trp Glu Gly Trp Glu Gly
                860                    865
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90

<210> 85
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 85
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<210> 86
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
 ggccagctat ctccgcag 18

<210> 87
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 87
 aagggcctgc aagagaag 18

<210> 88
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<220>
<223> Synthetic oligonucleotide probe

<400> 88
 cactgggaca actgtggg 18

<210> 89
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 89
 cagaggcaac gtggagag 18

<210> 90
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 90
 aagtattgtc atacagtgtt c 21

<210> 91
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 91
 tagtacttgg gcacgaggtt ggag 24

<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
 tcataccaac tgctggtcat tggc 24

<210> 93
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
 ctcaagctgc tggacacgga gcggccggtg aatcggtttc acttg 45

<210> 94
<211> 971
<212> DNA
<213> Homo sapiens

<400> 94
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 aaggagtgag gagctgctgg gcagagaggg actgtccggc tcccagatgc 100

 tgggcctcct ggggagcaca gccctcgtgg gatggatcac aggtgctgct 150

 gtggcggtcc tgctgctgct gctgctgctg gccacctgcc ttttccacgg 200

 acggcaggac tgtgacgtgg agaggaaccg tacagctgca gggggaaacc 250

 gagtccgccg ggcccagcct tggcccttcc ggcggcgggg ccacctggga 300

atctttcacc atcaccgtca tcctggccac gtatctcatg tgccgaatgt 350

gggcctccac caccaccacc accccgcca caccctcac cacctccacc 400

accaccacca ccccaccgc caccatcccc gccacgctcg ctgaggctgc 450

tgtcgccggt gcctgtggac agcagctgcc cctgccctcc catctgttcc 500

caggacaagt ggaccccatg tttccatgtg gaaggatgca tctctggggt 550

gaacgagggg aacaatagac tggggcttgc tccagctgca tttgcatggc 600

atgccccagt gtactatggc agcagagaat ggaggaacac tgggtctgca 650

gtgctgaagg gtttggggag tggagagcaa gggtgctctt tcggggctgg 700

acagcccgtc ttgtgacagt gactcccagt gagccccaga aatgacaagc 750

gtgtcttggc agagccagca cacaagtgga tgtgaagtgc ccgtcttgac 800

ctcctcatca ggctgctgca ggcctctggc gggcagggca ctgggagagg 850

ccctgagaat gtccttttgg tttggagaag gcagtgtgag gctgcacagt 900

caattcatcg gtgccttagt ccaagaaaat aaaaaccact aagaagcttt 950

aaaaaaaaaa aaaaaaaaa a 971

<210> 95
<211> 115
<212> PRT
<213> Homo sapiens

<400> 95
Met Leu Gly Leu Leu Gly Ser Thr Ala Leu Val Gly Trp Ile Thr
 1   5   10   15

Gly Ala Ala Val Ala Val Leu Leu Leu Leu Leu Leu Leu Ala Thr
                20   25   30

Cys Leu Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg
                35   40   45

Thr Ala Ala Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro
                50   55   60

Phe Arg Arg Arg Gly His Leu Gly Ile Phe His His His Arg His
                65   70   75

Pro Gly His Val Ser His Val Pro Asn Val Gly Leu His His His
                80   85   90

His His Pro Arg His Thr Pro His His Leu His His His His His
                95   100   105

Pro His Arg His His Pro Arg His Ala Arg
                110   115

93

<210> 96
<211> 1312
<212> DNA
<213> Homo sapiens

<400> 96
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tcggacctgc tactactggg cctgattggg ggcctgactc tcttactgct 100

gctgacgctg ctggcctttg ccgggtactc agggctactg gctggggtgg 150

aagtgagtgc tgggtcaccc cccatccgca acgtcactgt ggcctacaag 200

ttccacatgg ggctctatgg tgagactggg cggcttttca ctgagagctg 250

cagcatctct cccaagctcc gctccatcgc tgtctactat gacaacccc 300

acatggtgcc ccctgataag tgccgatgtg ccgtgggcag catcctgagt 350

gaaggtgagg aatcgccctc ccctgagctc atcgacctct accagaaatt 400

tggcttcaag gtgttctcct tcccggcacc cagccatgtg gtgacagcca 450

ccttccccta caccaccatt ctgtccatct ggctggctac ccgccgtgtc 500

catcctgcct tggacaccta catcaaggag cggaagctgt gtgcctatcc 550

tcggctggag atctaccagg aagaccagat ccatttcatg tgcccactgg 600

cacggcaggg agacttctat gtgcctgaga tgaaggagac agagtggaaa 650

tggcgggggc ttgtggaggc cattgacacc caggtggatg gcacaggagc 700

tgacacaatg agtgacacga gttctgtaag cttggaagtg agccctggca 750

gccgggagac ttcagctgcc acactgtcac ctggggcgag cagccgtggc 800

tgggatgacg gtgacacccg cagcgagcac agctacagcg agtcaggtgc 850

cagcggctcc tcttttgagg agctggactt ggagggcgag gggcccttag 900

gggagtcacg gctggaccct gggactgagc ccctggggac taccaagtgg 950

ctctgggagc ccactgcccc tgagaagggc aaggagtaac ccatggcctg 1000

caccctcctg cagtgcagtt gctgaggaac tgagcagact ctccagcaga 1050

ctctccagcc ctcttcctcc ttcctctggg ggaggagggg ttcctgaggg 1100

acctgacttc ccctgctcca ggcctcttgc taagccttct cctcactgcc 1150

ctttaggctc ccagggccag aggagccagg gactattttc tgcaccagcc 1200

cccagggctg ccgcccctgt tgtgtctttt tttcagactc acagtggagc 1250

ttccaggacc cagaataaag ccaatgattt acttgtttca cctggaaaaa 1300

94

aaaaaaaaaa aa 1312

<210> 97
<211> 313
<212> PRT
<213> Homo sapiens

<400> 97

Met	Ser	Asp	Leu	Leu	Leu	Leu	Gly	Leu	Ile	Gly	Gly	Leu	Thr	Leu
1				5					10					15

Leu Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly Leu
                20   25   30

Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
                35   40   45

Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr
                50   55   60

Gly Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg
                65   70   75

Ser Ile Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp
                80   85   90

Lys Cys Arg Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu Glu
                95   100   105

Ser Pro Ser Pro Glu Leu Ile Asp Leu Tyr Gln Lys Phe Gly Phe
                110   115   120

Lys Val Phe Ser Phe Pro Ala Pro Ser His Val Val Thr Ala Thr
                125   130   135

Phe Pro Tyr Thr Thr Ile Leu Ser Ile Trp Leu Ala Thr Arg Arg
                140   145   150

Val His Pro Ala Leu Asp Thr Tyr Ile Lys Glu Arg Lys Leu Cys
                155   160   165

Ala Tyr Pro Arg Leu Glu Ile Tyr Gln Glu Asp Gln Ile His Phe
                170   175   180

Met Cys Pro Leu Ala Arg Gln Gly Asp Phe Tyr Val Pro Glu Met
                185   190   195

Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val Glu Ala Ile Asp
                200   205   210

Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser Asp Thr Ser
                215   220   225

Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr Ser Ala
                230   235   240

Ala Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp Gly
                245   250   255

95

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Asp Thr Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly
                260             265             270

Ser Ser Phe Glu Glu Leu Asp Leu Glu Gly Glu Gly Pro Leu Gly
                275             280             285

Glu Ser Arg Leu Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys
                290             295             300

Trp Leu Trp Glu Pro Thr Ala Pro Glu Lys Gly Lys Glu
                305             310
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<210> 98
<211> 725
<212> DNA
<213> Homo sapiens

<400> 98

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ccccggctcc ctgccccgcg cccagtcatg accctgcgcc cctcactcct 100

cccgctccat ctgctgctgc tgctgctgct cagtgcggcg gtgtgccggg 150

ctgaggctgg gctcgaaacc gaaagtcccg tccggaccct ccaagtggag 200

accctggtgg agcccccaga accatgtgcc gagcccgctg cttttggaga 250

cacgcttcac atacactaca cgggaagctt ggtagatgga cgtattattg 300

acacctccct gaccagagac cctctggtta tagaacttgg ccaaaagcag 350

gtgattccag gtctggagca gagtcttctc gacatgtgtg tgggagagaa 400

gcgaagggca atcattcctt ctcacttggc ctatggaaaa cggggatttc 450

caccatctgt cccagcggat gcagtggtgc agtatgacgt ggagctgatt 500

gcactaatcc gagccaacta ctggctaaag ctggtgaagg catttttgcc 550

tctggtaggg atggccatgg tgccagccct cctgggcctc attgggtatc 600

acctatacag aaaggccaat agacccaaag tctccaaaaa gaagctcaag 650

gaagagaaac gaaacaagag caaaaagaaa taataaataa taaattttaa 700

aaaacttaaa aaaaaaaaa aaaaa 725
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<210> 99
<211> 201
<212> PRT
<213> Homo sapiens

<400> 99
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Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu
  1             5               10              15

Leu Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu
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96

Thr Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu
                    35   40   45

Pro Pro Glu Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu
                    50   55   60

His Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp
                    65   70   75

Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys
                    80   85   90

Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp Met Cys Val
                    95   100   105

Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala Tyr Gly
                    110   115   120

Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val Gln
                    125   130   135

Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg Ala Asn Tyr Trp Leu
                    140   145   150

Lys Leu Val Lys Gly Ile Leu Pro Leu Val Gly Met Ala Met Val
                    155   160   165

Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu Tyr Arg Lys Ala
                    170   175   180

Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu Glu Lys Arg
                    185   190   195

Asn Lys Ser Lys Lys Lys
                    200

<210> 100
<211> 705
<212> DNA
<213> Homo sapiens

<400> 100
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 ccggctccct gccccgcgcc cagtcatgac cctgcgcccc tcactcctcc 100

 cgctccatct gctgctgctg ctgctgctca gtgcggcggt gtgccgggct 150

 gaggctgggc tcgaaaccga aagtcccgtc cggaccctcc aagtggagac 200

 cctggtggag cccccagaac catgtgccga gccgctgct tttggagaca 250

 cgcttcacat acactacacg ggaagcttgg tagatggacg tattattgac 300

 acctccctga ccagagaccc tctggttata gaacttggcc aaaagcaggt 350

gattccaggt ctggagcaga gtcttctcga catgtgtgtg ggagagaagc 400

gaagggcaat cattccttct cacttggcct atggaaaacg gggatttcca 450

ccatctgtcc cagcggatgc agtggtgcag tatgacgtgg agctgattgc 500

actaatccga gccaactact ggctaaagct ggtgaagggc attttgcctc 550

tggtagggat ggccatggtg ccaccctcct gggcctcatt gggtatcacc 600

tatacagaaa ggccaataga cccaaagtct ccaaaaagaa gctcaaggaa 650

gagaaacgaa acaagagcaa aaagaaataa taaataataa attttaaaaa 700

actta 705

<210> 101
<211> 543
<212> DNA
<213> Homo sapiens

<400> 101
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 gaaccatgtg ccgagcccgc tgcttttgga gacacgcttc acatacacta 100

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 accctctggt tatagaactt ggccaaaagc aggtgattcc aggtctggag 200

 cagagtcttc tcgacatgtg tgtgggagag aagcgaaggg caatcattcc 250

 ttctcacttg gcctatggaa aacggggatt tccaccatct gtcccagcgg 300

 atgcagtggt gcagtatgac gtggagctga ttgcactaat ccgagccaac 350

 tactggctaa agctggtgaa gggcattttg cctctggtag ggatggccat 400

 ggtgccagcc tcctgggcc tcattgggta tcacctatac agaaaggcca 450

 atagacccaa agtctccaaa aagaagctca aggaagagaa acgaaacaag 500

 agcaaaaaga ataataaat aataaatttt aaaaaactta aaa 543

<210> 102
<211> 1316
<212> DNA
<213> Homo sapiens

<400> 102
 ctgctgcatc cgggtgtctg gaggctgtgg ccgttttgtt ttcttggcta 50

 aaatcggggg agtgaggcgg gccggcgcgg cgcgacaccg ggctccggaa 100

 ccactgcacg acggggctgg actgacctga aaaaaatgtc tggatttcta 150

 gagggcttga gatgctcaga atgcattgac tggggggaaa agcgcaatac 200

98

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tattgcttcc attgctgctg gtgtactatt ttttacaggc tggtggatta 250

tcatagatgc agctgttatt tatcccacca tgaaagattt caaccactca 300

taccatgcct gtggtgttat agcaaccata gccttcctaa tgattaatgc 350

agtatcgaat ggacaagtcc gaggtgatag ttacagtgaa ggttgtctgg 400

gtcaaacagg tgctcgcatt tggctttttcg ttggtttcat gttggccttt 450

ggatctctga ttgcatctat gtggattctt tttggaggtt atgttgctaa 500

agaaaaagac atagtatacc ctggaattgc tgtattttttc cagaatgcct 550

tcatctttttt tggagggctg gtttttaagt ttggccgcac tgaagactta 600

tggcagtgaa cacatctgat ttcccacagc acaacagccc tgcatgggtt 650

tgtttgtttt tttactgctc actcccaacc ttttgtaatg ccattttcta 700

aacttatttc tgagtgtagt ctcagcttaa agttgtgtaa tactaaaatc 750

acgagaacac ctaaacaaca accaaaaatc tattgtggta tgcacttgat 800

taacttataa aatgttagag gaaactttca catgaataat ttttgtcaaa 850

ttttatcatg gtataatttg taaaaataaa aagaaattac aaaagaaatt 900

atggatttgt caatgtaagt atttgtcata tctgaggtcc aaaaccacaa 950

tgaaagtgct ctgaagattt aatgtgttta ttcaaatgtg gtctcttctg 1000

tgtcaaatgt aaatgaaat ataaacattt tttagttttt aaaatattcc 1050

gtggtcaaaa ttcttcctca ctataattgg tatttacttt taccaaaaat 1100

tctgtgaaca tgtaatgtaa ctggcttttg agggtctccc aagggtgag 1150

tggacgtgtt ggaagagaga agcaccatgg tccagccacc aggctccctg 1200

tgtcccttcc atgggaaggt cttccgctgt gcctctcatt ccaagggcag 1250

gaagatgtga ctcagccatg acacgtggtt ctggtgggat gcacagtcac 1300

tccacatcca ccactg 1316
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<210> 103
<211> 157
<212> PRT
<213> Homo sapiens

<400> 103
Met Ser Gly Phe Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp
1   5   10   15

Trp Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val
                20   25   30

99

Leu Phe Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile
                35   40   45

Tyr Pro Thr Met Lys Asp Phe Asn His Ser Tyr His Ala Cys Gly
                50   55   60

Val Ile Ala Thr Ile Ala Phe Leu Met Ile Asn Ala Val Ser Asn
                65   70   75

Gly Gln Val Arg Gly Asp Ser Tyr Ser Glu Gly Cys Leu Gly Gln
                80   85   90

Thr Gly Ala Arg Ile Trp Leu Phe Val Gly Phe Met Leu Ala Phe
                95   100   105

Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Gly Tyr Val
               110   115   120

Ala Lys Glu Lys Asp Ile Val Tyr Pro Gly Ile Ala Val Phe Phe
               125   130   135

Gln Asn Ala Phe Ile Phe Phe Gly Gly Leu Val Phe Lys Phe Gly
               140   145   150

Arg Thr Glu Asp Leu Trp Gln
               155

<210> 104
<211> 545
<212> DNA
<213> Homo sapiens

<400> 104
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 ggctccggaa ccactgcacg acggggctgg actgacctga aaaaaatgtc 100

 tggatttcta gagggcttga gatgctcaga atgcattgac tggggggaaa 150

 agcgcaatac tattgcttcc attgctgctg gtgtactatt ttttacaggc 200

 tggtggatta tcatagatgc agctgttatt tatcccacca tgaaagattt 250

 caaccactca taccatgcct gtggtgttat agcaaccata gccttcctaa 300

 tgattaatgc agtatcgaat ggacaagtcc gaggtgatag ttacagtgaa 350

 ggttgtctgg gtcaaacagg tgctcgcatt tggcttttcg ttggtttcat 400

 gttggccttt ggatctctga ttgcatctat gtggattctt tttggaggtt 450

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 cagaatgcct tcatcttttt tggagggctg gttttaagt ttggc 545

<210> 105
<211> 490
<212> DNA

100

<213> Homo sapiens

<220>
<221> unsure
<222> 31, 39, 108, 145, 179, 219, 412, 479
<223> unknown base

<400> 105
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 agaatgcatg actgggggaa aagcgcaaat actattgctt ccattgctgc 100

 tggtgtanta ttttttacag gctggtggat tatcatagat gcagntgtta 150

 tttatcccac catgaaagat ttcaaccant cataccatgc ctgtggtgtt 200

 atagcaacca tagccttcnt aatgattaat gcagtatcga atggacaagt 250

 ccgaggtgat agttacagtg aaggttgttt gggtcaaaca ggtgctcgca 300

 tttggctttt cgttggtttc atgttggcct ttggatctct gattgcatct 350

 atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 400

 ccctggaatt gntgtatttt tccagaatgc cttcatcttt tttggagggc 450

 tggtttttaa gtttggccgc actgaagant tatggcagtg 490

<210> 106
<211> 466
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 26, 38, 81, 115, 207, 329, 380, 446, 449
<223> unknown base

<400> 106
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 aatgtttgga tttttagagg gcttgagatg ntcagaatgc attgactggg 100

 ggaaaagcgc aatantattg ctttccattg ctgctggtgt actatttttt 150

 acagggtggt ggattatcat agatgcagct gttatttatc ccaccatgaa 200

 agatttnaac cactcatacc atgcctgtgg tgttatagca accatagcct 250

 tcctaatgat taatgcagta tcgaatggac aagtccgagg tgatagttac 300

 agtgaaggtt gtttgggtca acaggtgnt cgcatttggc ttttcgttgg 350

 tttcatgttg gcctttggat ttctgattgn attctatgcg gattcttctt 400

 ggaggttatg ttgctaaaga aaaagacata gtataccctg gaattnctnt 450

 attttttccag aatgcc 466

<210> 107
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 52, 67, 70, 78, 105, 144, 150, 209, 266, 268, 282, 310, 331, 356
<223> unknown base

<400> 107
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antattgctt ccattgntgn tggtgtanta tttttttaca ggctggtgga 100

ttatnataga tgcagctgtt atttatccca ccatgaaaga tttnaaccan 150

tcataccatg cctgtggtgt tatagcaacc atagccttcc taatgattaa 200

tgcagtatng aatggacaag tccgaggtga tagttacagt gaaggttgtt 250

tgggtcaaac aggtgntngc atttggcttt tngttggttt catgttggcc 300

tttggatctn tgattgcatt tatgtggatt nttttggag gttatgttgc 350

taaagnaaaa gacatagtat accctgt 377

<210> 108
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 12, 25, 65, 130, 437, 537
<223> unknown base

<400> 108
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ggcccggcgc ggcgngacac cgggttccgg gaaccattgc acgacggggt 100

ggactgacct gaaaaaaatg tttggatttn tagagggctt gagatgctca 150

gaatgcattg actgggggga aaagcgcaat actattgctt ccattgctgc 200

tggtgtacta tttttttacag gctggtggat tatcatagat gcagctgtta 250

tttatcccac catgaaagat ttcaaccact cataccatgc ctgtggtgtt 300

atagcaacca tagccttcct aatgattaat gcagtatcga atggacaagt 350

ccgaggtgat agttacagtg aaggttgtct gggtcaaaca ggtgctcgca 400

tttggctttt cgttggtttc atgttggcct ttggatntct gattgcatct 450

atgtggattc ttttggagg ttatgttgct aaagaaaaag acatagtata 500

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ccctggaatt gctgtatttt tccagaatgc cttcatnttt tttggagggc 550

 tg 552

<210> 109
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 109
 gggtggatgg tactgctgca tcc 23

<210> 110
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 110
 tgttgtgctg tgggaaatca gatgtg 26

<210> 111
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 111
 gtgtctggag gctgtggccg ttttgttttc ttgggctaaa atcggg 46

<210> 112
<211> 3004
<212> DNA
<213> Homo sapiens

<400> 112
 cgacgccggc gtgatgtggc ttccgctggt gctgctcctg gctgtgctgc 50

 tgctggccgt cctctgcaaa gtttacttgg gactattctc tggcagctcc 100

 ccgaatcctt tctccgaaga tgtcaaacgg cccccagcgc ccctggtaac 150

 tgacaaggag gccaggaaga aggttctcaa acaagctttt tcagccaacc 200

 aagtgccgga gaagctggat gtggtggtaa ttggcagtgg ctttgggggc 250

 ctggctgcag ctgcaattct agctaaagct ggcaagcgag tcctggtgct 300

 ggaacaacat accaaggcag ggggctgctg tcataccttt ggaaagaatg 350

 gccttgaatt tgacacagga atccattaca ttgggcgtat ggaagagggc 400
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103

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agcattggcc gttttatctt ggaccagatc actgaagggc agctggactg 450

ggctcccctg tcctctcctt ttgacatcat ggtactggaa gggcccaatg 500

gccgaaagga gtaccccatg tacagtggag agaaagccta cattcagggc 550

ctcaaggaga agtttccaca ggaggaagct atcattgaca agtatataaa 600

gctggttaag gtggtatcca gtggagcccc tcatgccatc ctgttgaaat 650

tcctcccatt gcccgtggtt cagctcctcg acaggtgtgg ctgctgact 700

cgtttctctc cattccttca agcatccacc cagagcctgg ctgaggtcct 750

gcagcagctg ggggcctcct ctgagctcca ggcagtactc agctacatct 800

tccccactta cggtgtcacc cccaaccaca gtgccttttc catgcacgcc 850

ctgctggtca accactacat gaaaggaggc ttttatcccc gagggggttc 900

cagtgaaatt gccttccaca ccatccctgt gattcagcgg ctgggggcg 950

ctgtcctcac aaaggccact gtgcagagtg tgttgctgga ctcagctggg 1000

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tactgccggg gaacgcccgc tgcctgccag gtgtgaagca gcaactgggg 1150

acggtgcggc ccggcttagg catgacctct gttttcatct gcctgcgagg 1200

caccaaggaa gacctgcatc tgccgtccac caactactat gtttactatg 1250

acacggacat ggaccaggcg atggagcgct acgtctccat gcccagggaa 1300

gaggctgcgg aacacatccc tcttctcttc ttcgctttcc catcagccaa 1350

agatccgacc tgggaggacc gattcccagg ccggtccacc atgatcatgc 1400

tcatacccac tgcctacgag tggtttgagg agtggcaggc ggagctgaag 1450

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agagtgtgac tgcaggatcc ccactcacca accagttcta tctggctgct 1600

ccccgaggtg cctgctacgg ggctgaccat gacctgggcc gcctgcaccc 1650

ttgtgtgatg gcctccttga gggcccagag ccccatcccc aacctctatc 1700

tgacaggcca ggatatcttc acctgtggac tggtcggggc cctgcaaggt 1750

gccctgctgt gcagcagcgc catcctgaag cggaacttgt actcagacct 1800

taagaatctt gattctagga tccgggcaca gaagaaaaag aattagttcc 1850
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104

atcagggagg agtcagagga atttgcccaa tggctggggc atctcccttg 1900

acttacccat aatgtctttc tgcattagtt ccttgcacgt ataaagcact 1950

ctaatttggt tctgatgcct gaagagaggc ctagtttaaa tcacaattcc 2000

gaatctgggg caatggaatc actgcttcca gctggggcag gtgagatctt 2050

tacgcctttt ataacatgcc atccctacta ataggatatt gacttggata 2100

gcttgatgtc tcatgacgag cggcgctctg catccctcac ccatgcctcc 2150

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gtgttgtcag ctcaacctgg tgggttcagt tctgtcctga ggcttctgct 2250

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gcaggctgca gggcattcca gccaagggca cagcagggga cagtgcaggg 2750

aggtgtgggg taagggaggg aagtcacatc agaaaaggga aagccacgga 2800

atgtgtgtga agcccagaaa tggcatttgc agttaattag cacatgtgag 2850

ggttagacag gtaggtgaat gcaagctcaa ggtttggaaa aatgactttt 2900

cagttatgtc tttggtatca gacatacgaa aggtctcttt gtagttcgtg 2950

ttaatgtaac attaataaat ttattgattc cattgcttta aaaaaaaaaa 3000

aaaa 3004

<210> 113
<211> 610
<212> PRT
<213> Homo sapiens

<400> 113
Met Trp Leu Pro Leu Val Leu Leu Leu Ala Val Leu Leu Leu Ala
 1   5   10   15

Val Leu Cys Lys Val Tyr Leu Gly Leu Phe Ser Gly Ser Ser Pro

105

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                 20                      25                      30
Asn Pro Phe Ser Glu Asp Val Lys Arg Pro Pro Ala Pro Leu Val
                35                      40                      45

Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser
                50                      55                      60

Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser
                65                      70                      75

Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly
                80                      85                      90

Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys
                95                      100                     105

Cys His Thr Phe Gly Lys Asn Gly Leu Glu Phe Asp Thr Gly Ile
                110                     115                     120

His Tyr Ile Gly Arg Met Glu Glu Gly Ser Ile Gly Arg Phe Ile
                125                     130                     135

Leu Asp Gln Ile Thr Glu Gly Gln Leu Asp Trp Ala Pro Leu Ser
                140                     145                     150

Ser Pro Phe Asp Ile Met Val Leu Glu Gly Pro Asn Gly Arg Lys
                155                     160                     165

Glu Tyr Pro Met Tyr Ser Gly Glu Lys Ala Tyr Ile Gln Gly Leu
                170                     175                     180

Lys Glu Lys Phe Pro Gln Glu Glu Ala Ile Ile Asp Lys Tyr Ile
                185                     190                     195

Lys Leu Val Lys Val Val Ser Ser Gly Ala Pro His Ala Ile Leu
                200                     205                     210

Leu Lys Phe Leu Pro Leu Pro Val Val Gln Leu Leu Asp Arg Cys
                215                     220                     225

Gly Leu Leu Thr Arg Phe Ser Pro Phe Leu Gln Ala Ser Thr Gln
                230                     235                     240

Ser Leu Ala Glu Val Leu Gln Gln Leu Gly Ala Ser Ser Glu Leu
                245                     250                     255

Gln Ala Val Leu Ser Tyr Ile Phe Pro Thr Tyr Gly Val Thr Pro
                260                     265                     270

Asn His Ser Ala Phe Ser Met His Ala Leu Leu Val Asn His Tyr
                275                     280                     285

Met Lys Gly Gly Phe Tyr Pro Arg Gly Gly Ser Ser Glu Ile Ala
                290                     295                     300

Phe His Thr Ile Pro Val Ile Gln Arg Ala Gly Gly Ala Val Leu
                305                     310                     315
```

106

Thr Lys Ala Thr Val Gln Ser Val Leu Leu Asp Ser Ala Gly Lys
                320   325   330

Ala Cys Gly Val Ser Val Lys Lys Gly His Glu Leu Val Asn Ile
                335   340   345

Tyr Cys Pro Ile Val Val Ser Asn Ala Gly Leu Phe Asn Thr Tyr
                350   355   360

Glu His Leu Leu Pro Gly Asn Ala Arg Cys Leu Pro Gly Val Lys
                365   370   375

Gln Gln Leu Gly Thr Val Arg Pro Gly Leu Gly Met Thr Ser Val
                380   385   390

Phe Ile Cys Leu Arg Gly Thr Lys Glu Asp Leu His Leu Pro Ser
                395   400   405

Thr Asn Tyr Tyr Val Tyr Tyr Asp Thr Asp Met Asp Gln Ala Met
                410   415   420

Glu Arg Tyr Val Ser Met Pro Arg Glu Glu Ala Ala Glu His Ile
                425   430   435

Pro Leu Leu Phe Phe Ala Phe Pro Ser Ala Lys Asp Pro Thr Trp
                440   445   450

Glu Asp Arg Phe Pro Gly Arg Ser Thr Met Ile Met Leu Ile Pro
                455   460   465

Thr Ala Tyr Glu Trp Phe Glu Glu Trp Gln Ala Glu Leu Lys Gly
                470   475   480

Lys Arg Gly Ser Asp Tyr Glu Thr Phe Lys Asn Ser Phe Val Glu
                485   490   495

Ala Ser Met Ser Val Val Leu Lys Leu Phe Pro Gln Leu Glu Gly
                500   505   510

Lys Val Glu Ser Val Thr Ala Gly Ser Pro Leu Thr Asn Gln Phe
                515   520   525

Tyr Leu Ala Ala Pro Arg Gly Ala Cys Tyr Gly Ala Asp His Asp
                530   535   540

Leu Gly Arg Leu His Pro Cys Val Met Ala Ser Leu Arg Ala Gln
                545   550   555

Ser Pro Ile Pro Asn Leu Tyr Leu Thr Gly Gln Asp Ile Phe Thr
                560   565   570

Cys Gly Leu Val Gly Ala Leu Gln Gly Ala Leu Leu Cys Ser Ser
                575   580   585

Ala Ile Leu Lys Arg Asn Leu Tyr Ser Asp Leu Lys Asn Leu Asp
                590   595   600

Ser Arg Ile Arg Ala Gln Lys Lys Lys Asn

107

<210> 114
<211> 1701
<212> DNA
<213> Homo sapiens

<400> 114
gcagcggcga ggcggcggtg gtggctgagt ccgtggtggc agaggcgaag 50

gcgacagctc taggggttgg caccggcccc gagaggagga tgcgggtccg 100

gatagggctg acgctgctgc tgtgtgcggt gctgctgagc ttggcctcgg 150

cgtcctcgga tgaagaaggc agccaggatg aatccttaga ttccaagact 200

actttgacat cagatgagtc agtaaaggac catactactg caggcagagt 250

agttgctggt caaatatttc ttgattcaga agaatctgaa ttagaatcct 300

ctattcaaga agaggaagac agcctcaaga gccaagaggg ggaaagtgtc 350

acagaagata tcagctttct agagtctcca aatccagaaa acaaggacta 400

tgaagagcca aagaaagtac ggaaaccagc tttgaccgcc attgaaggca 450

cagcacatgg ggagccctgc cacttccctt ttctttttcct agataaggag 500

tatgatgaat gtacatcaga tgggagggaa gatggcagac tgtggtgtgc 550

tacaacctat gactacaaag cagatgaaaa gtggggcttt tgtgaaactg 600

aagaagaggc tgctaagaga cggcagatgc aggaagcaga aatgatgtat 650

caaactggaa tgaaaatcct taatggaagc aataagaaaa gccaaaaaag 700

agaagcatat cggtatctcc aaaaggcagc aagcatgaac cataccaaag 750

ccctggagag agtgtcatat gctctttttat ttggtgatta cttgccacag 800

aatatccagg cagcgagaga gatgtttgag aagctgactg aggaaggctc 850

tcccaaggga cagactgctc ttggctttct gtatgcctct ggacttggtg 900

ttaattcaag tcaggcaaag gctcttgtat attatacatt tggagctctt 950

gggggcaatc taatagccca catggttttg gtaagtagac tttagtggaa 1000

ggctaataat attaacatca gaagaatttg tggtttatag cggccacaac 1050

tttttcagct ttcatgatcc agatttgctt gtattaagac caaatattca 1100

gttgaacttc cttcaaattc ttgttaatgg atataacaca tggaatctac 1150

atgtaaatga aagttggtgg agtccacaat ttttctttaa aatgattagt 1200

ttggctgatt gcccctaaaa agagagatct gataaatggc tcttttttaaa 1250

ttttctctga gttggaattg tcagaatcat tttttacatt agattatcat 1300

aattttaaaa attttctttt agtttttcaa aatttgtaa atggtggcta 1350

tagaaaaaca acatgaaata ttatacaata ttttgcaaca atgccctaag 1400

aattgttaaa attcatggag ttatttgtgc agaatgactc cagagagctc 1450

tactttctgt tttttacttt tcatgattgg ctgtcttccc atttattctg 1500

gtcatttatt gctagtgaca ctgtgcctgc ttccagtagt ctcattttcc 1550

ctattttgct aatttgttac tttttctttg ctaatttgga agattaactc 1600

attttaata aaattatgtc taagattaaa aaaaaaaaa aaaaaaaaa 1650

aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1700

a 1701

<210> 115
<211> 301
<212> PRT
<213> Homo sapiens

<400> 115
Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Cys Ala Val Leu
 1   5   10   15

Leu Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp
                20   25   30

Glu Ser Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val
                35   40   45

Lys Asp His Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe
                50   55   60

Leu Asp Ser Glu Glu Ser Glu Leu Glu Ser Ser Ile Gln Glu Glu
                65   70   75

Glu Asp Ser Leu Lys Ser Gln Glu Gly Glu Ser Val Thr Glu Asp
                80   85   90

Ile Ser Phe Leu Glu Ser Pro Asn Pro Glu Asn Lys Asp Tyr Glu
                95   100   105

Glu Pro Lys Lys Val Arg Lys Pro Ala Leu Thr Ala Ile Glu Gly
                110   115   120

Thr Ala His Gly Glu Pro Cys His Phe Pro Phe Leu Phe Leu Asp
                125   130   135

Lys Glu Tyr Asp Glu Cys Thr Ser Asp Gly Arg Glu Asp Gly Arg
                140   145   150

Leu Trp Cys Ala Thr Thr Tyr Asp Tyr Lys Ala Asp Glu Lys Trp
                155   160   165

109

Gly Phe Cys Glu Thr Glu Glu Glu Ala Ala Lys Arg Arg Gln Met
                170   175   180

Gln Glu Ala Glu Met Met Tyr Gln Thr Gly Met Lys Ile Leu Asn
                185   190   195

Gly Ser Asn Lys Lys Ser Gln Lys Arg Glu Ala Tyr Arg Tyr Leu
                200   205   210

Gln Lys Ala Ala Ser Met Asn His Thr Lys Ala Leu Glu Arg Val
                215   220   225

Ser Tyr Ala Leu Leu Phe Gly Asp Tyr Leu Pro Gln Asn Ile Gln
                230   235   240

Ala Ala Arg Glu Met Phe Glu Lys Leu Thr Glu Glu Gly Ser Pro
                245   250   255

Lys Gly Gln Thr Ala Leu Gly Phe Leu Tyr Ala Ser Gly Leu Gly
                260   265   270

Val Asn Ser Ser Gln Ala Lys Ala Leu Val Tyr Tyr Thr Phe Gly
                275   280   285

Ala Leu Gly Gly Asn Leu Ile Ala His Met Val Leu Val Ser Arg
                290   295   300

Leu

<210> 116
<211> 584
<212> DNA
<213> Homo sapiens

<400> 116
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 ttctacttgc ctgcctccct gcctctggcc atggcctgcc ggtgcctcag 100

 cttccttctg atggggacct cctgtcagt ttcccagaca gtcctggccc 150

 agctggatgc actgctggtc ttcccaggcc aagtggctca actctcctgc 200

 acgctcagcc cccagcacgt caccatcagg gactacggtg tgtcctggta 250

 ccagcagcgg gcaggcagtg cccctcgata tctcctctac taccgctcgg 300

 aggaggatca ccaccggcct gctgacatcc ccgatcgatt ctcggcagcc 350

 aaggatgagg cccacaatgc ctgtgtcctc accattagtc ccgtgcagcc 400

 tgaagacgac gcggattact actgctctgt tggctacggc tttagtccct 450

 aggggtgggg tgtgagatgg gtgcctcccc tctgcctccc atttctgccc 500

 ctgaccttgg gtccctttta aactttctct gagccttgct tcccctctgt 550

aaaatgggtt aataatattc aacatgtcaa caac 584

<210> 117
<211> 123
<212> PRT
<213> Homo sapiens

<400> 117
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Met Ala Cys Arg Cys Leu Ser Phe Leu Leu Met Gly Thr Phe Leu
 1               5                  10                  15

Ser Val Ser Gln Thr Val Leu Ala Gln Leu Asp Ala Leu Leu Val
                20                  25                  30

Phe Pro Gly Gln Val Ala Gln Leu Ser Cys Thr Leu Ser Pro Gln
                35                  40                  45

His Val Thr Ile Arg Asp Tyr Gly Val Ser Trp Tyr Gln Gln Arg
                50                  55                  60

Ala Gly Ser Ala Pro Arg Tyr Leu Leu Tyr Tyr Arg Ser Glu Glu
                65                  70                  75

Asp His His Arg Pro Ala Asp Ile Pro Asp Arg Phe Ser Ala Ala
                80                  85                  90

Lys Asp Glu Ala His Asn Ala Cys Val Leu Thr Ile Ser Pro Val
                95                  100                 105

Gln Pro Glu Asp Asp Ala Asp Tyr Tyr Cys Ser Val Gly Tyr Gly
                110                 115                 120

Phe Ser Pro
```

<210> 118
<211> 3402
<212> DNA
<213> Homo sapiens

<400> 118
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gccgccccgc cccgagaccg ggcccggggg cgcggggcgg cgggatgcgg 50

cgcccggggc ggcgatgacc gcggagcgca cgccgcgggc ccggccctga 100

ccccgccgcc cgcccgctga gccccccgcc gaggtccgga caggccgaga 150

tgacgccgag cccctgttg ctgctcctgc tgccgccgct gctgctgggg 200

gccttcccac cggccgccgc cgcccgaggc cccccaaaga tggcggacaa 250

ggtggtccca cggcaggtgg cccggctggg ccgcactgtg cggctgcagt 300

gcccagtgga gggggacccg ccgccgctga ccatgtggac caaggatggc 350

cgcaccatcc acagcggctg gagccgcttc cgcgtgctgc cgcaggggct 400

gaaggtgaag caggtggagc gggaggatgc cggcgtgtac gtgtgcaagg 450
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111

ccaccaacgg cttcggcagc ctgagcgtca actacaccct cgtcgtgctg 500

gatgacatta gcccagggaa ggagagcctg gggcccgaca gctcctctgg 550

gggtcaagag gaccccgcca gccagcagtg ggcacgaccg cgcttcacac 600

agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc 650

gtgcggctca agtgcgtggc cagcgggcac cctcggcccg acatcacgtg 700

gatgaaggac gaccaggcct tgacgcgccc agaggccgct gagcccagga 750

agaagaagtg gacactgagc ctgaagaacc tgcggccgga ggacagcggc 800

aaatacacct gccgcgtgtc gaaccgcgcg ggcgccatca cgccaccta 850

caaggtggat gtgatccagc ggacccgttc caagcccgtg ctcacaggca 900

cgcaccccgt gaacacgacg gtggacttcg ggggaccac gtccttccag 950

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ccagacaggc agactgggag gatggaggac ggagctgcag acgaaggcag 1750

gggacccatg gcgaggagga atggccagca ccccaggcag tctgtgtgtg 1800

aggcatagcc cctggacaca cacacacaga cacacacact acctggatgc 1850

atgtatgcac acacatgcgc gcacacgtgc tccctgaagg cacacgtacg 1900

112

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cacacgcaca tgcacagata tgccgcctgg gcacacagat aagctgccca 1950

aatgcacgca cacgcacaga gacatgccag aacatacaag gacatgctgc 2000

ctgaacatac acacgcacac ccatgcgcag atgtgctgcc tggacacaca 2050

cacacacacg gatatgctgt ctggacgcac acacgtgcag atatggtatc 2100

cggacacaca cgtgcacaga tatgctgcct ggacacacag ataatgctgc 2150

cttgacacac acatgcacgg atattgcctg gacacacaca cacacacg 2200

cgtgcacaga tatgctgtct ggacacgcac acacatgcag atatgctgcc 2250

tggacacaca cttccagaca cacgtgcaca ggcgcagata tgctgcctgg 2300

acacacgcag atatgctgtc tagtcacaca cacacgcaga catgctgtcc 2350

ggacacacac acgcatgcac agatatgctg tccggacaca cacacgcacg 2400

cagatatgct gcctggacac acacacagat aatgctgcct caacactcac 2450

acacgtgcag atattgcctg gacacacaca tgtgcacaga tatgctgtct 2500

ggacatgcac acacgtgcag atatgctgtc cggatacaca cgcacgcaca 2550

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cccatggcta gtggctcatc cccagtgcat tctcccctg acacagagaa 3150

ggggccttgg tatttatatt taagaaatga agataatatt aataatgatg 3200

gaaggaagac tgggttgcag ggactgtggt ctctcctggg gcccgggacc 3250

cgcctggtct ttcagccatg ctgatgacca caccccgtcc aggccagaca 3300

ccaccccca ccccactgtc gtggtggccc cagatctctg taattttatg 3350
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113

tagagtttga gctgaagccc cgtatattta atttattttg ttaaacacaa 3400

aa 3402

<210> 119
<211> 504
<212> PRT
<213> Homo sapiens

<400> 119

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu
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Leu Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys
                20              25                  30

Met Ala Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg
                35                  40                  45

Thr Val Arg Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu
                50                  55                  60

Thr Met Trp Thr Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser
                65                  70                  75

Arg Phe Arg Val Leu Pro Gln Gly Leu Lys Val Lys Gln Val Glu
                80                  85                  90

Arg Glu Asp Ala Gly Val Tyr Val Cys Lys Ala Thr Asn Gly Phe
                95                  100                 105

Gly Ser Leu Ser Val Asn Tyr Thr Leu Val Val Leu Asp Asp Ile
                110                 115                 120

Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly
                125                 130                 135

Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr
                140                 145                 150

Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly
                155                 160                 165

Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
                170                 175                 180

Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu
                185                 190                 195

Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn
                200                 205                 210

Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn
                215                 220                 225

Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln
                230                 235                 240
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114

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Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
              245             250             255

Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val
              260             265             270

Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu
              275             280             285

Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly
              290             295             300

Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro
              305             310             315

Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
              320             325             330

Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
              335             340             345

Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys
              350             355             360

Pro Pro Gly Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu
              365             370             375

Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile
              380             385             390

Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro
              395             400             405

Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro
              410             415             420

Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu
              425             430             435

Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His
              440             445             450

Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val
              455             460             465

Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
              470             475             480

His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys
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Val His Gln His Ile His Tyr Gln Cys
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115

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<223> Synthetic oligonucleotide probe

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<210> 122
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

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<210> 123
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<212> DNA
<213> Homo sapiens

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 gcctgggtgt tctccttcct ggtcctggaa gtcacatctg tgttggggag 200

 acagacgatg ctcacccagt cagtaagaag agtccagcct gggaagaaga 250

 accccagcat ctttgccaag cctgccgaca ccctggagag ccctggtgag 300

 tggacaacat ggttcaacat cgactaccca ggcgggaagg gcgactatga 350

 gcggctggac gccattcgct ctactatgg ggaccgtgta tgtgcccgtc 400

 ccctgcggct agaggctcgg accactgact ggacacctgc gggcagcact 450

 ggccaggtgg tccatggtag tccccgtgag ggtttctggt gcctcaacag 500

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 gcccaccagg atccctgcgc cgagacacag agcgcatctg gagcccatgg 600

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cagggctgc tatctacctc ctgaccaaga cgccgaagct gctgacccag 900

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tcggaaagag cccatcactt tggaagccat ggagaccaac atcatccccc 1900

tgggggaagt ggttggtgaa gaccccatgg ctgaactgga gattccatcc 1950

aggagtttct acaggcagaa tggggagccc tacataggaa aagtgaaggc 2000

cagtgtgacc ttcctggatc cccggaatat ttccacagcc acagctgccc 2050
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117

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tgccagagca catatccaca gtgaaactct ggtcactcaa tccagacaca 2250

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caccctggtg aaggtcatcc cccagggcag ctgccgtcga gccagtgtga 3250

accccatgct gcatgagtac ctggtcaacc acttgccact tgcagtcaac 3300

aacgacacca gtgagtacac catgctggca cccttggacc cactgggcca 3350

caactatggc atctacactg tcactgacca ggaccctcgc acggccaagg 3400

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atcatgaaga gcaatgtggg agtagccctc accttcaact gtgtagagag 3500
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118

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cagcgagcga gcaggggtgg ccagcgccag ggtggagtgg tggcctctct 3650

gagatttcct agagttgctc aacagcccct gatcaactaa gttttgtggt 3700

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tgcacaaact gtcacttggt taatttaagc acttctgttt tcgtgaattt 3800

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catggttttg cccacctctg caatagtgat aatctgatgc tgaagatcaa 4050

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<212> PRT
<213> Homo sapiens

<400> 124
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                20                  25                  30

Arg Arg Val Gln Pro Gly Lys Lys Asn Pro Ser Ile Phe Ala Lys
                35                  40                  45

Pro Ala Asp Thr Leu Glu Ser Pro Gly Glu Trp Thr Thr Trp Phe
                50                  55                  60

Asn Ile Asp Tyr Pro Gly Gly Lys Gly Asp Tyr Glu Arg Leu Asp
                65                  70                  75
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119

Ala Ile Arg Phe Tyr Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu
                    80   85   90

Arg Leu Glu Ala Arg Thr Thr Asp Trp Thr Pro Ala Gly Ser Thr
                95   100   105

Gly Gln Val Val His Gly Ser Pro Arg Glu Gly Phe Trp Cys Leu
                110   115   120

Asn Arg Glu Gln Arg Pro Gly Gln Asn Cys Ser Asn Tyr Thr Val
                125   130   135

Arg Phe Leu Cys Pro Pro Gly Ser Leu Arg Arg Asp Thr Glu Arg
                140   145   150

Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys Cys Ser Ala Ala Cys
                155   160   165

Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile Cys Leu Ala Glu
                170   175   180

Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly Gln His Cys
                185   190   195

Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro Met Gly
                200   205   210

Gln Val Asn Ala Asp Cys Asp Ala Cys Met Cys Gln Asp Phe Met
                215   220   225

Leu His Gly Ala Val Ser Leu Pro Gly Gly Ala Pro Ala Ser Gly
                230   235   240

Ala Ala Ile Tyr Leu Leu Thr Lys Thr Pro Lys Leu Leu Thr Gln
                245   250   255

Thr Asp Ser Asp Gly Arg Phe Arg Ile Pro Gly Leu Cys Pro Asp
                260   265   270

Gly Lys Ser Ile Leu Lys Ile Thr Lys Val Lys Phe Ala Pro Ile
                275   280   285

Val Leu Thr Met Pro Lys Thr Ser Leu Lys Ala Ala Thr Ile Lys
                290   295   300

Ala Glu Phe Val Arg Ala Glu Thr Pro Tyr Met Val Met Asn Pro
                305   310   315

Glu Thr Lys Ala Arg Arg Ala Gly Gln Ser Val Ser Leu Cys Cys
                320   325   330

Lys Ala Thr Gly Lys Pro Arg Pro Asp Lys Tyr Phe Trp Tyr His
                335   340   345

Asn Asp Thr Leu Leu Asp Pro Ser Leu Tyr Lys His Glu Ser Lys
                350   355   360

Leu Val Leu Arg Lys Leu Gln Gln His Gln Ala Gly Glu Tyr Phe

120

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                365                    370                    375
Cys Lys Ala Gln Ser Asp Ala Gly Ala Val Lys Ser Lys Val Ala
            380                385                    390
Gln Leu Ile Val Thr Ala Ser Asp Glu Thr Pro Cys Asn Pro Val
            395                400                    405
Pro Glu Ser Tyr Leu Ile Arg Leu Pro His Asp Cys Phe Gln Asn
            410                415                    420
Ala Thr Asn Ser Phe Tyr Tyr Asp Val Gly Arg Cys Pro Val Lys
            425                430                    435
Thr Cys Ala Gly Gln Gln Asp Asn Gly Ile Arg Cys Arg Asp Ala
            440                445                    450
Val Gln Asn Cys Cys Gly Ile Ser Lys Thr Glu Glu Arg Glu Ile
            455                460                    465
Gln Cys Ser Gly Tyr Thr Leu Pro Thr Lys Val Ala Lys Glu Cys
            470                475                    480
Ser Cys Gln Arg Cys Thr Glu Thr Arg Ser Ile Val Arg Gly Arg
            485                490                    495
Val Ser Ala Ala Asp Asn Gly Glu Pro Met Arg Phe Gly His Val
            500                505                    510
Tyr Met Gly Asn Ser Arg Val Ser Met Thr Gly Tyr Lys Gly Thr
            515                520                    525
Phe Thr Leu His Val Pro Gln Asp Thr Glu Arg Leu Val Leu Thr
            530                535                    540
Phe Val Asp Arg Leu Gln Lys Phe Val Asn Thr Thr Lys Val Leu
            545                550                    555
Pro Phe Asn Lys Lys Gly Ser Ala Val Phe His Glu Ile Lys Met
            560                565                    570
Leu Arg Arg Lys Glu Pro Ile Thr Leu Glu Ala Met Glu Thr Asn
            575                580                    585
Ile Ile Pro Leu Gly Glu Val Val Gly Glu Asp Pro Met Ala Glu
            590                595                    600
Leu Glu Ile Pro Ser Arg Ser Phe Tyr Arg Gln Asn Gly Glu Pro
            605                610                    615
Tyr Ile Gly Lys Val Lys Ala Ser Val Thr Phe Leu Asp Pro Arg
            620                625                    630
Asn Ile Ser Thr Ala Thr Ala Ala Gln Thr Asp Leu Asn Phe Ile
            635                640                    645
Asn Asp Glu Gly Asp Thr Phe Pro Leu Arg Thr Tyr Gly Met Phe
            650                655                    660
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121

Ser Val Asp Phe Arg Asp Glu Val Thr Ser Glu Pro Leu Asn Ala
                665   670   675

Gly Lys Val Lys Val His Leu Asp Ser Thr Gln Val Lys Met Pro
                680   685   690

Glu His Ile Ser Thr Val Lys Leu Trp Ser Leu Asn Pro Asp Thr
                695   700   705

Gly Leu Trp Glu Glu Glu Gly Asp Phe Lys Phe Glu Asn Gln Arg
                710   715   720

Arg Asn Lys Arg Glu Asp Arg Thr Phe Leu Val Gly Asn Leu Glu
                725   730   735

Ile Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Ser Arg
                740   745   750

Arg Cys Phe Val Lys Val Arg Ala Tyr Arg Ser Glu Arg Phe Leu
                755   760   765

Pro Ser Glu Gln Ile Gln Gly Val Val Ile Ser Val Ile Asn Leu
                770   775   .   780

Glu Pro Arg Thr Gly Phe Leu Ser Asn Pro Arg Ala Trp Gly Arg
                785   790   795

Phe Asp Ser Val Ile Thr Gly Pro Asn Gly Ala Cys Val Pro Ala
                800   805   810

Phe Cys Asp Asp Gln Ser Pro Asp Ala Tyr Ser Ala Tyr Val Leu
                815   820   825

Ala Ser Leu Ala Gly Glu Glu Leu Gln Ala Val Glu Ser Ser Pro
                830   835   840

Lys Phe Asn Pro Asn Ala Ile Gly Val Pro Gln Pro Tyr Leu Asn
                845   850   855

Lys Leu Asn Tyr Arg Arg Thr Asp His Glu Asp Pro Arg Val Lys
                860   865   870

Lys Thr Ala Phe Gln Ile Ser Met Ala Lys Pro Arg Pro Asn Ser
                875   880   885

Ala Glu Glu Ser Asn Gly Pro Ile Tyr Ala Phe Glu Asn Leu Arg
                890   895   900

Ala Cys Glu Glu Ala Pro Pro Ser Ala Ala His Phe Arg Phe Tyr
                905   910   915

Gln Ile Glu Gly Asp Arg Tyr Asp Tyr Asn Thr Val Pro Phe Asn
                920   925   930

Glu Asp Asp Pro Met Ser Trp Thr Glu Asp Tyr Leu Ala Trp Trp
                935   940   945

Pro Lys Pro Met Glu Phe Arg Ala Cys Tyr Ile Lys Val Lys Ile

122

Val Gly Pro Leu Glu Val Asn Val Arg Ser Arg Asn Met Gly Gly
                965   970   975

Thr His Arg Arg Thr Val Gly Lys Leu Tyr Gly Ile Arg Asp Val
                980   985   990

Arg Ser Thr Arg Asp Arg Asp Gln Pro Asn Val Ser Ala Ala Cys
                995   1000   1005

Leu Glu Phe Lys Cys Ser Gly Met Leu Tyr Asp Gln Asp Arg Val
               1010   1015   1020

Asp Arg Thr Leu Val Lys Val Ile Pro Gln Gly Ser Cys Arg Arg
               1025   1030   1035

Ala Ser Val Asn Pro Met Leu His Glu Tyr Leu Val Asn His Leu
               1040   1045   1050

Pro Leu Ala Val Asn Asn Asp Thr Ser Glu Tyr Thr Met Leu Ala
               1055   1060   1065

Pro Leu Asp Pro Leu Gly His Asn Tyr Gly Ile Tyr Thr Val Thr
               1070   1075   1080

Asp Gln Asp Pro Arg Thr Ala Lys Glu Ile Ala Leu Gly Arg Cys
               1085   1090   1095

Phe Asp Gly Thr Ser Asp Gly Ser Ser Arg Ile Met Lys Ser Asn
               1100   1105   1110

Val Gly Val Ala Leu Thr Phe Asn Cys Val Glu Arg Gln Val Gly
               1115   1120   1125

Arg Gln Ser Ala Phe Gln Tyr Leu Gln Ser Thr Pro Ala Gln Ser
               1130   1135   1140

Pro Ala Ala Gly Thr Val Gln Gly Arg Val Pro Ser Arg Arg Gln
               1145   1150   1155

Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Gly Gly Val Val Ala
               1160   1165   1170

Ser Leu Arg Phe Pro Arg Val Ala Gln Gln Pro Leu Ile Asn
               1175   1180

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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 125
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<210> 126
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 126
 ccattgtgca ggtcaggtca cag 23

<210> 127
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<212> DNA
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<211> 2819
<212> DNA
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 ctacctaccc gtacgcatac atacatatgt gtatatatat gtaaactaga 200

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 gacaacatag ttattacctt tgaatctggg cgtccagacc aaatgatcct 750

124

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taacagcccc ctctaaaagc gcaagccagt catacccctg tatatcttag 2200
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125

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gctttaacac tggaagattt aaagaataaa aactcctgca taaacgattt 2600

caggaatttg tattgcaatt tcttaagatg aaaggaacag ccaccaagca 2650

gtttcacact cactttactg atttctgtgt ggactgagta cattcagctg 2700

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<211> 438
<212> PRT
<213> Homo sapiens

<400> 129
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Val Ser Ser Val Met Gln Pro Tyr Pro Leu Val Trp Gly His Tyr
                20   25   30

Asp Leu Cys Lys Thr Gln Ile Tyr Thr Glu Gly Lys Val Trp
                35   40   45

Asp Tyr Met Ala Cys Gln Pro Glu Ser Thr Asp Met Thr Lys Tyr
                50   55   60

Leu Lys Val Lys Leu Asp Pro Pro Asp Ile Thr Cys Gly Asp Pro
                65   70   75

Pro Glu Thr Phe Cys Ala Met Gly Asn Pro Tyr Met Cys Asn Asn
                80   85   90

Glu Cys Asp Ala Ser Thr Pro Glu Leu Ala His Pro Pro Glu Leu
                95   100   105

Met Phe Asp Phe Glu Gly Arg His Pro Ser Thr Phe Trp Gln Ser
                110   115   120

Ala Thr Trp Lys Glu Tyr Pro Lys Pro Leu Gln Val Asn Ile Thr
                125   130   135

126

Leu Ser Trp Ser Lys Thr Ile Glu Leu Thr Asp Asn Ile Val Ile
                140   145   150

Thr Phe Glu Ser Gly Arg Pro Asp Gln Met Ile Leu Glu Lys Ser
                155   160   165

Leu Asp Tyr Gly Arg Thr Trp Gln Pro Tyr Gln Tyr Tyr Ala Thr
                170   175   180

Asp Cys Leu Asp Ala Phe His Met Asp Pro Lys Ser Val Lys Asp
                185   190   195

Leu Ser Gln His Thr Val Leu Glu Ile Ile Cys Thr Glu Glu Tyr
                200   205   210

Ser Thr Gly Tyr Thr Thr Asn Ser Lys Ile Ile His Phe Glu Ile
                215   220   225

Lys Asp Arg Phe Ala Leu Phe Ala Gly Pro Arg Leu Arg Asn Met
                230   235   240

Ala Ser Leu Tyr Gly Gln Leu Asp Thr Thr Lys Lys Leu Arg Asp
                245   250   255

Phe Phe Thr Val Thr Asp Leu Arg Ile Arg Leu Leu Arg Pro Ala
                260   265   270

Val Gly Glu Ile Phe Val Asp Glu Leu His Leu Ala Arg Tyr Phe
                275   280   285

Tyr Ala Ile Ser Asp Ile Lys Val Arg Gly Arg Cys Lys Cys Asn
                290   295   300

Leu His Ala Thr Val Cys Val Tyr Asp Asn Ser Lys Leu Thr Cys
                305   310   315

Glu Cys Glu His Asn Thr Thr Gly Pro Asp Cys Gly Lys Cys Lys
                320   325   330

Lys Asn Tyr Gln Gly Arg Pro Trp Ser Pro Gly Ser Tyr Leu Pro
                335   340   345

Ile Pro Lys Gly Thr Ala Asn Thr Cys Ile Pro Ser Ile Ser Ser
                350   355   360

Ile Gly Thr Asn Val Cys Asp Asn Glu Leu Leu His Cys Gln Asn
                365   370   375

Gly Gly Thr Cys His Asn Asn Val Arg Cys Leu Cys Pro Ala Ala
                380   385   390

Tyr Thr Gly Ile Leu Cys Glu Lys Leu Arg Cys Glu Glu Ala Gly
                395   400   405

Ser Cys Gly Ser Asp Ser Gly Gln Gly Ala Pro Pro His Gly Thr
                410   415   420

Pro Ala Leu Leu Leu Leu Thr Thr Leu Leu Gly Thr Ala Ser Pro

127

Leu Val Phe

<210> 130
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 130
 tcgattatgg acgaacatgg cagc 24

<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 131
 ttctgagatc cctcatcctc 20

<210> 132
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 132
 aggttcaggg acagcaagtt tggg 24

<210> 133
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 133
 tttgctggac ctcggctacg gaattggctt ccctctacgg acagctggat 50

<210> 134
<211> 1493
<212> DNA
<213> Homo sapiens

<400> 134
 cccacgcgtc cgggtgacct gggccgagcc ctcccggtcg gctaagattg 50

 ctgaggaggc ggcgggtagc tggcaggcgc cgacttccga aggccgccgt 100

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ccgggcgagg tgtcctcatg acttctcttg tggaccatgt ccgtgatctt 150

ttttgcctgc gtggtacggg taagggatgg actgcccctc tcagcctcta 200

ctgattttta ccacacccaa gattttttgg aatggaggag acggctcaag 250

agtttagcct tgcgactggc ccagtatcca ggtcgaggtt ctgcagaagg 300

ttgtgacttt agtatacatt tttcttcttt cggggacgtg gcctgcatgg 350

ctatctgctc ctgccagtgt ccagcagcca tggccttctg cttcctggag 400

accctgtggt gggaattcac agcttcctat gacactacct gcattggcct 450

agcctccagg ccatacgctt ttcttgagtt tgacagcatc attcagaaag 500

tgaagtggca ttttaactat gtaagttcct ctcagatgga gtgcagcttg 550

gaaaaaattc aggaggagct caagttgcag cctccagcgg ttctcactct 600

ggaggacaca gatgtggcaa atggggtgat gaatggtcac acaccgatgc 650

acttggagcc tgctcctaat ttccgaatgg aaccagtgac agccctgggt 700

atcctctccc tcattctcaa catcatgtgt gctgccctga atctcattcg 750

aggagttcac cttgcagaac attctttaca ggatccaagg agctggttct 800

gctggttgga ccaaacctcg tgagccagcc acccctgacc caaatgagga 850

gagctctgat tctcccatcc gggagcagtg atgtcaaact tctgctgctg 900

gggaaatctc atcagcaggg agcctgtgga aaagggcatg tcagtgaaat 950

ctgggaatgg ctggattcgg aaacatctgc ccatgtgtat tgatggcaga 1000

gctgttgccc acaagcgcct tttatttagg gtaaaattaa caaatccatt 1050

ctattcctct gacccatgct tagtacatat gacctttaac ccttacattt 1100

atatgattct ggggttgctt cagaagtgtt atttcatgaa tcattcatat 1150

gatttgatcc cccaggattc tattttgttt aatgggcttt tctactaaaa 1200

gcataaaata ctgaggctga tttagtcagg gcaaaaccat ttactttaca 1250

tattcgtttt caatacttgc tgttcatgtt acacaagctt cttacggttt 1300

tcttgtaaca ataaatattt tgagtaaata atgggtacat tttaacaaac 1350

tcagtagtac aacctaaact tgtataaaag tgtgtaaaaa tgtatagcca 1400

tttatatcct atgtataaat taaatgaggt ggcttcagaa atggcagaat 1450

aaatctaaag tgtttattaa aaaaaaaaaa aaaaaaaaaa aag 1493
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<210> 135
<211> 228

129

<212> PRT
<213> Homo sapiens

<400> 135
Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly
1   5   10   15

Leu Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe
                20   25   30

Leu Glu Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Ala
                35   40   45

Gln Tyr Pro Gly Arg Gly Ser Ala Glu Gly Cys Asp Phe Ser Ile
                50   55   60

His Phe Ser Ser Phe Gly Asp Val Ala Cys Met Ala Ile Cys Ser
                65   70   75

Cys Gln Cys Pro Ala Ala Met Ala Phe Cys Phe Leu Glu Thr Leu
                80   85   90

Trp Trp Glu Phe Thr Ala Ser Tyr Asp Thr Thr Cys Ile Gly Leu
                95   100   105

Ala Ser Arg Pro Tyr Ala Phe Leu Glu Phe Asp Ser Ile Ile Gln
                110   115   120

Lys Val Lys Trp His Phe Asn Tyr Val Ser Ser Ser Gln Met Glu
                125   130   135

Cys Ser Leu Glu Lys Ile Gln Glu Glu Leu Lys Leu Gln Pro Pro
                140   145   150

Ala Val Leu Thr Leu Glu Asp Thr Asp Val Ala Asn Gly Val Met
                155   160   165

Asn Gly His Thr Pro Met His Leu Glu Pro Ala Pro Asn Phe Arg
                170   175   180

Met Glu Pro Val Thr Ala Leu Gly Ile Leu Ser Leu Ile Leu Asn
                185   190   195

Ile Met Cys Ala Ala Leu Asn Leu Ile Arg Gly Val His Leu Ala
                200   205   210

Glu His Ser Leu Gln Asp Pro Arg Ser Trp Phe Cys Trp Leu Asp
                215   220   225

Gln Thr Ser

<210> 136
<211> 239
<212> DNA
<213> Homo sapiens

<220>

130

<221> unsure
<222> 39, 61, 143, 209
<223> unknown base

<400> 136
 tgcttcctgg agaccctgtg gtgggaattc acagcttcnt atgacactac 50

 ctgcattggc ntagcctcca ggccatacgc ttttcttgag tttgacagca 100

 tcattcagaa agtgaagtgg cattttaact atgtaagttc ctntcagatg 150

 gagtgcagct tggaaaaaat tcaggaggag ctcaagttgc agcctccagc 200

 ggttctcant atggaggaca cagatgtggc aaatggggt 239

<210> 137
<211> 2300
<212> DNA
<213> Homo sapiens

<400> 137
 ctcagcggcg cttcctcgta gcgagcctag tggcgggtgt ttgcattgaa 50

 acgtgagcgc gacccgacct taaagagtgg ggagcaaagg gaggacagag 100

 ccctttaaaa cgaggcgggt ggtgcctgcc cctttaaggg cggggcgtcc 150

 ggacgactgt atctgagccc cagactgccc cgagtttctg tcgcaggctg 200

 cgaggaaagg cccctaggct gggtctgggt gcttggcggc ggcggcttcc 250

 tccccgctcg tcctccccgg gcccagaggc acctcggctt cagtcatgct 300

 gagcagagta tggaagcacc tgactacgaa gtgctatccg tgcgagaaca 350

 gctattccac gagaggatcc gcgagtgtat tatatcaaca cttctgtttg 400

 caacactgta catcctctgc cacatcttcc tgacccgctt caagaagcct 450

 gctgagttca ccacagtgga tgatgaagat gccaccgtca acaagattgc 500

 gctcgagctg tgcaccttta ccctggcaat tgccctgggt gctgtcctgc 550

 tcctgccctt ctccatcatc agcaatgagg tgctgctctc cctgcctcgg 600

 aactactaca tccagtggct caacggctcc ctcatccatg gcctctggaa 650

 ccttgttttt ctcttcccca acctgtccct catcttcctc atgccctttg 700

 catatttctt cactgagtct gagggctttg ctggctccag aaagggtgtc 750

 ctgggccggg tctatgagac agtggtgatg ttgatgctcc tcactctgct 800

 ggtgctaggt atggtgtggg tggcatcagc cattgtggac aagaacaagg 850

 ccaacagaga gtcactctat gactttgggg agtactatct cccctacctc 900

 tactcatgca tctccttcct tggggttctg ctgctcctgg tgtgtactcc 950

131

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actgggtctc gcccgcatgt tctccgtcac tgggaagctg ctagtcaagc 1000

cccggctgct ggaagacctg gaggagcagc tgtactgctc agcctttgag 1050

gaggcagccc tgacccgcag gatctgtaat cctacttcct gctggctgcc 1100

tttagacatg gagctgctac acagacaggt cctggctctg cagacacaga 1150

gggtcctgct ggagaagagg cggaaggctt cagcctggca acggaacctg 1200

ggctacccc tggctatgct gtgcttgctg gtgctgacgg gcctgtctgt 1250

gctcattgtg gccatccaca tcctggagct gctcatcgat gaggctgcca 1300

tgccccgagg catgcagggt acctccttag gccaggtctc cttctccaag 1350

ctgggctcct ttggtgccgt cattcaggtt gtactcatct tttacctaat 1400

ggtgtcctca gttgtgggct tctatagctc tccactcttc cggagcctgc 1450

ggcccagatg gcacgacact gccatgacgc agataattgg gaactgtgtc 1500

tgtctcctgg tcctaagctc agcacttcct gtcttctctc gaaccctggg 1550

gctcactcgc tttgacctgc tgggtgactt tggacgcttc aactggctgg 1600

gcaatttcta cattgtgttc ctctacaacg cagcctttgc aggcctcacc 1650

acactctgtc tggtgaagac cttcactgca gctgtgcggg cagagctgat 1700

ccgggccttt gggctggaca gactgccgct gcccgtctcc ggtttccccc 1750

aggcatctag gaagacccag caccagtgac ctccagctgg gggtgggaag 1800

gaaaaaactg gacactgcca tctgctgcct aggcctggag ggaagcccaa 1850

ggctacttgg acctcaggac ctggaatctg agagggtggg tggcagaggg 1900

gagcagagcc atctgcacta ttgcataatc tgagccagag tttgggacca 1950

ggacctcctg cttttccata cttaactgtg gcctcagcat ggggtagggc 2000

tgggtgactg ggtctagccc ctgatcccaa atctgtttac acatcaatct 2050

gcctcactgc tgttctgggc catccccata gccatgttta catgatttga 2100

tgtgcaatag ggtggggtag gggcagggaa aggactgggc cagggcaggc 2150

tcgggagata gattgtctcc cttgcctctg gcccagcaga gcctaagcac 2200

tgtgctatcc tggaggggct ttggaccacc tgaaagacca aggggatagg 2250

gaggaggagg cttcagccat cagcaataaa gttgatccca gggaaaaaaa 2300
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<210> 138
<211> 489
<212> PRT
<213> Homo sapiens

132

<400> 138

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Met Glu Ala Pro Asp Tyr Glu Val Leu Ser Val Arg Glu Gln Leu
 1               5                  10                      15

Phe His Glu Arg Ile Arg Glu Cys Ile Ile Ser Thr Leu Leu Phe
                20              25                      30

Ala Thr Leu Tyr Ile Leu Cys His Ile Phe Leu Thr Arg Phe Lys
                35              40                      45

Lys Pro Ala Glu Phe Thr Thr Val Asp Asp Glu Asp Ala Thr Val
                50              55                      60

Asn Lys Ile Ala Leu Glu Leu Cys Thr Phe Thr Leu Ala Ile Ala
                65              70                      75

Leu Gly Ala Val Leu Leu Leu Pro Phe Ser Ile Ile Ser Asn Glu
                80              85                      90

Val Leu Leu Ser Leu Pro Arg Asn Tyr Tyr Ile Gln Trp Leu Asn
                95              100                     105

Gly Ser Leu Ile His Gly Leu Trp Asn Leu Val Phe Leu Phe Pro
                110             115                     120

Asn Leu Ser Leu Ile Phe Leu Met Pro Phe Ala Tyr Phe Phe Thr
                125             130                     135

Glu Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val Leu Gly Arg
                140             145                     150

Val Tyr Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val
                155             160                     165

Leu Gly Met Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn Lys
                170             175                     180

Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro
                185             190                     195

Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu Leu Leu Leu
                200             205                     210

Val Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val Thr Gly
                215             220                     225

Lys Leu Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu Gln
                230             235                     240

Leu Tyr Cys Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile
                245             250                     255

Cys Asn Pro Thr Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu
                260             265                     270

His Arg Gln Val Leu Ala Leu Gln Thr Gln Arg Val Leu Leu Glu
                275             280                     285
```

133

```
Lys Arg Arg Lys Ala Ser Ala Trp Gln Arg Asn Leu Gly Tyr Pro
              290                 295                 300

Leu Ala Met Leu Cys Leu Leu Val Leu Thr Gly Leu Ser Val Leu
              305                 310                 315

Ile Val Ala Ile His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala
              320                 325                 330

Met Pro Arg Gly Met Gln Gly Thr Ser Leu Gly Gln Val Ser Phe
              335                 340                 345

Ser Lys Leu Gly Ser Phe Gly Ala Val Ile Gln Val Val Leu Ile
              350                 355                 360

Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro
              365                 370                 375

Leu Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr
              380                 385                 390

Gln Ile Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala
              395                 400                 405

Leu Pro Val Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu
              410                 415                 420

Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile
              425                 430                 435

Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr Thr Leu Cys
              440                 445                 450

Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu Ile Arg
              455                 460                 465

Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe Pro
              470                 475                 480

Gln Ala Ser Arg Lys Thr Gln His Gln
              485
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<210> 139
<211> 294
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 53, 57
<223> unknown base

<400> 139
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ggctgccgag ggaaggcccc ttgggttggt cttggttgct tggcggcggc 50

ggnttcntcc ccgctcgtcc tccccgggcc cagaggcacc tcggcttcag 100

tcatgctgag cagagtatgg aagcacctga ctacgaagtg ctatccgtgc 150
```

134

gagaacagct attccacgag aggatccgcg agtgtattat atcaacactt 200

ctgtttgcaa cactgtacat cctctgccac atcttcctga cccgcttcaa 250

gaagcctgct gagttcacca cagtggatga tgaagatgcc accg 294

<210> 140
<211> 526
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 197, 349
<223> unknown base

<400> 140
gaccgacctt aaagagtggg agcaaaggga ggacagagcc ttttaaaacg 50

aggcggtggt gcctgccctt taagggcggg gcgtccggac gactgtatct 100

gagccccaga ctgccccgag tttctgtcgc aggctgcgag gaaaggcccc 150

taggctgggt ctggtgcttg gcggcggcgg cttcctcccc gttgtcntcc 200

ccgggcccag aggcacctcg gcttcagtca tgctgagcag agtatggaag 250

cacctgacta cgaagtgcta tccgtgcgag aacagctatt ccacgagagg 300

atccgcgagt gtattatatc aacacttctg tttgcaacac tgtacatcnt 350

ctgccacatc ttcctgaccc gcttcaagaa gcctgctgag ttcaccacag 400

tggatgatga agatgccacc gtcaacaaga ttgcgctcga gctgtgcacc 450

tttaccctgg caattgccct gggtgctgtc ctgctcctgc ccttctccat 500

catcagcaat gaggtgctgc actccc 526

<210> 141
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
gactgtatct gagccccaga ctgc 24

<210> 142
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
 tcagcaatga ggtgctgctc 20

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
 tgaggaagat gagggacagg ttgg 24

<210> 144
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 144
 tatggaagca cctgactacg aagtgctatc cgtgcgagaa cagctattcc 50

<210> 145
<211> 685
<212> DNA
<213> Homo sapiens

<400> 145
 gatgtgctcc ttggagctgg tgtgcagtgt cctgactgta agatcaagtc 50

 caaacctgtt ttggaattga ggaaacttct cttttgatct cagcccttgg 100

 tggtccaggt cttcatgctg ctgtgggtga tattactggt cctggctcct 150

 gtcagtggac agtttgcaag gacacccagg cccattattt tcctccagcc 200

 tccatggacc acagtcttcc aaggagagag agtgaccctc acttgcaagg 250

 gatttcgctt ctactcacca cagaaaacaa aatggtacca tcggtacctt 300

 gggaaagaaa tactaagaga aaccccagac aatatccttg aggttcagga 350

 atctggagag tacagatgcc aggcccaggg ctccctctc agtagccctg 400

 tgcacttgga tttttcttca gagatgggat ttcctcatgc tgcccaggct 450

 aatgttgaac tcctgggctc aagtgatctg ctcacctagg cctctcaaag 500

 cgctgggatt acagcttcgc tgatcctgca agctccactt tctgtgtttg 550

 aaggagactc tgtggttctg aggtgccggg caaaggcgga agtaacactg 600

 aataatacta tttacaagaa tgataatgtc ctggcattcc ttaataaaag 650

 aactgacttc caaaaaaaaa aaaaaaaaa aaaaa 685

<210> 146
<211> 124
<212> PRT
<213> Homo sapiens

<400> 146
Met Leu Leu Trp Val Ile Leu Leu Val Leu Ala Pro Val Ser Gly
 1   5   10   15

Gln Phe Ala Arg Thr Pro Arg Pro Ile Ile Phe Leu Gln Pro Pro
                20   25   30

Trp Thr Thr Val Phe Gln Gly Glu Arg Val Thr Leu Thr Cys Lys
                35   40   45

Gly Phe Arg Phe Tyr Ser Pro Gln Lys Thr Lys Trp Tyr His Arg
                50   55   60

Tyr Leu Gly Lys Glu Ile Leu Arg Glu Thr Pro Asp Asn Ile Leu
                65   70   75

Glu Val Gln Glu Ser Gly Glu Tyr Arg Cys Gln Ala Gln Gly Ser
                80   85   90

Pro Leu Ser Ser Pro Val His Leu Asp Phe Ser Ser Glu Met Gly
                95   100   105

Phe Pro His Ala Ala Gln Ala Asn Val Glu Leu Leu Gly Ser Ser
                110   115   120

Asp Leu Leu Thr

<210> 147
<211> 1621
<212> DNA
<213> Homo sapiens

<400> 147
cagaagaggg ggctagctag ctgtctctgc ggaccaggga accccccgcg 50

cccccccggt gtgaggcggc ctcacagggc cgggtgggct ggcgagccga 100

cgcggcggcg gaggaggctg tgaggagtgt gtggaacagg acccgggaca 150

gaggaaccat ggctccgcag aacctgagca ccttttgcct gttgctgcta 200

tacctcatcg gggcggtgat tgccggacga gatttctata agatcttggg 250

ggtgcctcga agtgcctcta taaggatat taaaaaggcc tataggaaac 300

tagccctgca gcttcatccc gaccggaacc ctgatgatcc acaagcccag 350

gagaaattcc aggatctggg tgctgcttat gaggttctgt cagatagtga 400

gaaacggaaa cagtacgata cttatggtga agaaggatta aaagatggtc 450

atcagagctc ccatggagac attttttcac acttctttgg ggattttggt 500

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ttcatgtttg gaggaacccc tcgtcagcaa gacagaaata ttccaagagg 550

aagtgatatt attgtagatc tagaagtcac tttggaagaa gtatatgcag 600

gaaattttgt ggaagtagtt agaaacaaac ctgtggcaag gcaggctcct 650

ggcaaacgga agtgcaattg tcggcaagag atgcggacca cccagctggg 700

ccctgggcgc ttccaaatga cccaggaggt ggtctgcgac gaatgcccta 750

atgtcaaact agtgaatgaa gaacgaacgc tggaagtaga aatagagcct 800

ggggtgagag acggcatgga gtaccccttt attggagaag gtgagcctca 850

cgtggatggg gagcctggag atttacggtt ccgaatcaaa gttgtcaagc 900

acccaatatt tgaaaggaga ggagatgatt tgtacacaaa tgtgacaatc 950

tcattagttg agtcactggt tggctttgag atggatatta ctcacttgga 1000

tggtcacaag gtacatattt cccgggataa gatcaccagg ccaggagcga 1050

agctatggaa gaaagggaa gggctcccca actttgacaa caacaatatc 1100

aagggctctt tgataatcac ttttgatgtg gattttccaa aagaacagtt 1150

aacagaggaa gcgagagaag gtatcaaaca gctactgaaa caagggtcag 1200

tgcagaaggt atacaatgga ctgcaaggat attgagagtg aataaaattg 1250

gactttgttt aaaataagtg aataagcgat atttattatc tgcaaggttt 1300

ttttgtgtgt gttttttgttt ttatttttcaa tatgcaagtt aggcttaatt 1350

tttttatcta atgatcatca tgaaatgaat aagagggctt aagaatttgt 1400

ccatttgcat tcggaaaaga atgaccagca aaaggtttac taatacctct 1450

cccttttgggg atttaatgtc tggtgctgcc gcctgagttt caagaattaa 1500

agctgcaaga ggactccagg agcaaaagaa acacaatata gagggttgga 1550

gttgttagca atttcattca aaatgccaac tggagaagtc tgtttttaaa 1600

tacattttgt tgttattttt a 1621
```

<210> 148
<211> 358
<212> PRT
<213> Homo sapiens

<400> 148

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Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr
1               5                   10                  15

Leu Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu
            20                  25                  30
```

138

Gly Val Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr
             35   40   45

Arg Lys Leu Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp
             50   55   60

Pro Gln Ala Gln Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu
             65   70   75

Val Leu Ser Asp Ser Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly
             80   85   90

Glu Glu Gly Leu Lys Asp Gly His Gln Ser Ser His Gly Asp Ile
             95   100   105

Phe Ser His Phe Phe Gly Asp Phe Gly Phe Met Phe Gly Gly Thr
             110   115   120

Pro Arg Gln Gln Asp Arg Asn Ile Pro Arg Gly Ser Asp Ile Ile
             125   130   135

Val Asp Leu Glu Val Thr Leu Glu Glu Val Tyr Ala Gly Asn Phe
             140   145   150

Val Glu Val Val Arg Asn Lys Pro Val Ala Arg Gln Ala Pro Gly
             155   160   165

Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg Thr Thr Gln Leu
             170   175   180

Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu
             185   190   195

Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu Glu Val
             200   205   210

Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe Ile
             215   220   225

Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
             230   235   240

Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly
             245   250   255

Asp Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu
             260   265   270

Val Gly Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val
             275   280   285

His Ile Ser Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp
             290   295   300

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys
             305   310   315

Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln

139

Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln
            335   340   345

Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr
            350   355

<210> 149
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,
      482
<223> unknown base

<400> 149
 tgggaccagg gaaccccggg cccccggtg gagngcctaa caggccggtg 50

 gntgcgaccg aagcggcggg cggaggaggt tttgaggatt tttggaacag 100

 gacccggaca gaggaaccat ggttccgcag aacntgagca cnttttgcct 150

 gttgntgnta tacttcatcg gggcggtgat tgccggacga gatttntata 200

 agattttggg gtgcctngaa gtgccttnta taaaggatat taaaaaggcc 250

 tataggaaac tagccctgca gntttatccc gaccggaacc ctgatgatcc 300

 acaagcccag gagaaattcc aggatttggg tgctgcttat gaggttntgt 350

 cagatagtga gaaacggaaa cagtacgata attatggtga gaaggatta 400

 aaagatggtn atcagagctc ccatggagac attttttcac acttntttgg 450

 ggattttggt ttcatgtttg gaggaacccc tngtcagcaa gacagaaata 500

 ttccaagag 509

<210> 150
<211> 1532
<212> DNA
<213> Homo sapiens

<400> 150
 ggcacgaggc ggcggggcag tcgcgggatg cgcccgggag ccacagcctg 50

 aggccctcag gtctctgcag gtgtcgtgga ggaacctagc acctgccatc 100

 ctcttcccca atttgccact ccagcagct ttagcccatg aggaggatgt 150

 gaccgggact gagtcaggag ccctctggaa gcatggagac tgtggtgatt 200

 gttgccatag gtgtgctggc caccatcttt ctggcttcgt ttgcagcctt 250

140

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ggtgctggtt tgcaggcagc gctactgccg gccgcgagac ctgctgcagc 300

gctatgattc taagcccatt gtggacctca ttggtgccat ggagacccag 350

tctgagccct ctgagttaga actggacgat gtcgttatca ccaacccccca 400

cattgaggcc attctggaga atgaagactg gatcgaagat gcctcgggtc 450

tcatgtccca ctgcattgcc atcttgaaga tttgtcacac tctgacagag 500

aagcttgttg ccatgacaat gggctctggg gccaagatga agacttcagc 550

cagtgtcagc gacatcattg tggtggccaa gcggatcagc cccagggtgg 600

atgatgttgt gaagtcgatg taccctccgt tggaccccaa actcctggac 650

gcacggacga ctgccctgct cctgtctgtc agtcacctgg tgctggtgac 700

aaggaatgcc tgccatctga cgggaggcct ggactggatt gaccagtctc 750

tgtcggctgc tgaggagcat ttggaagtcc ttcgagaagc agccctagct 800

tctgagccag ataaaggcct cccaggccct gaaggcttcc tgcaggagca 850

gtctgcaatt tagtgcctac aggccagcag ctagccatga aggcccctgc 900

cgccatccct ggatggctca gcttagcctt ctactttttc ctatagagtt 950

agttgttctc cacggctgga gagttcagct gtgtgtgcat agtaaagcag 1000

gagatccccg tcagtttatg cctcttttgc agttgcaaac tgtggctggt 1050

gagtggcagt ctaatactac agttagggga gatgccattc actctctgca 1100

agaggagtat tgaaaactgg tggactgtca gctttattta gctcacctag 1150

tgttttcaag aaaattgagc caccgtctaa gaaatcaaga ggtttcacat 1200

taaaattaga atttctggcc tctctcgatc ggtcagaatg tgtggcaatt 1250

ctgatctgca ttttcagaag aggacaatca attgaaacta agtaggggtt 1300

tcttcttttg gcaagacttg tactctctca cctggcctgt ttcatttatt 1350

tgtattatct gcctggtccc tgaggcgtct gggtctctcc tctcccttgc 1400

aggtttgggt ttgaagctga ggaactacaa agttgatgat ttctttttta 1450

tctttatgcc tgcaatttta cctagctacc actaggtgga tagtaaattt 1500

atacttatgt ttccctcaaa aaaaaaaaaa aa 1532
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<210> 151
<211> 226
<212> PRT
<213> Homo sapiens

<400> 151

141

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Met Glu Thr Val Val Ile Val Ala Ile Gly Val Leu Ala Thr Ile
 1               5                  10                  15

Phe Leu Ala Ser Phe Ala Ala Leu Val Leu Val Cys Arg Gln Arg
               20                  25                  30

Tyr Cys Arg Pro Arg Asp Leu Leu Gln Arg Tyr Asp Ser Lys Pro
               35                  40                  45

Ile Val Asp Leu Ile Gly Ala Met Glu Thr Gln Ser Glu Pro Ser
               50                  55                  60

Glu Leu Glu Leu Asp Asp Val Val Ile Thr Asn Pro His Ile Glu
               65                  70                  75

Ala Ile Leu Glu Asn Glu Asp Trp Ile Glu Asp Ala Ser Gly Leu
               80                  85                  90

Met Ser His Cys Ile Ala Ile Leu Lys Ile Cys His Thr Leu Thr
               95                 100                 105

Glu Lys Leu Val Ala Met Thr Met Gly Ser Gly Ala Lys Met Lys
              110                 115                 120

Thr Ser Ala Ser Val Ser Asp Ile Ile Val Val Ala Lys Arg Ile
              125                 130                 135

Ser Pro Arg Val Asp Asp Val Val Lys Ser Met Tyr Pro Pro Leu
              140                 145                 150

Asp Pro Lys Leu Leu Asp Ala Arg Thr Thr Ala Leu Leu Leu Ser
              155                 160                 165

Val Ser His Leu Val Leu Val Thr Arg Asn Ala Cys His Leu Thr
              170                 175                 180

Gly Gly Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala Ala Glu Glu
              185                 190                 195

His Leu Glu Val Leu Arg Glu Ala Ala Leu Ala Ser Glu Pro Asp
              200                 205                 210

Lys Gly Leu Pro Gly Pro Glu Gly Phe Leu Gln Glu Gln Ser Ala
              215                 220                 225

Ile

<210> 152
<211> 1027
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1017, 1020
<223> unknown base
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<400> 152
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tcgccgctgt ccccaccact gcagccatga tctccttaac ggacacgcag 100

aaaattggaa tgggattaac aggatttgga gtgttttcc tgttctttgg 150

aatgattctc tttttgaca aagcactact ggctattgga aatgttttat 200

ttgtagccgg cttggctttt gtaattggtt tagaaagaac attcagattc 250

ttcttccaaa aacataaaat gaaagctaca ggttttttc tgggtggtgt 300

atttgtagtc cttattggtt ggcctttgat aggcatgatc ttcgaaattt 350

atggattttt tctcttgttc aggggcttct ttcctgtcgt tgttggcttt 400

attagaagag tgccagtcct tggatccctc ctaaatttac ctggaattag 450

atcatttgta gataaagttg gagaaagcaa caatatggta taacaacaag 500

tgaatttgaa gactcattta aaatattgtg ttatttataa agtcatttga 550

agaatattca gcacaaaatt aaattacatg aaatagcttg taatgttctt 600

tacaggagtt taaaacgtat agcctacaaa gtaccagcag caaattagca 650

aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 700

caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc 750

ttgaaggcta tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc 800

ttagagaact gtggtgcctg tttcttttct ttttattttg aaggctcagg 850

agcatccata ggcatttgct ttttagaagt gtccactgca atggcaaaaa 900

tatttccagt tgcactgtat ctctggaagt gatgcatgaa ttcgattgga 950

ttgtgtcatt ttaaagtatt aaaaccaagg aaaccccaat tttgatgtat 1000

ggattacttt tttttgngcn cagggcc 1027
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<210> 153
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> N-myristoylation Sites
<222> 11-16, 51-56 and 116-121
<223> N-myristoylation Sites.

<220>
<221> Transmembrane domains
<222> 12-30, 33-52, 69-89 and 93-109
<223> Transmembrane domains

<220>
<221> Aminoacyl-transfer RNA Synthetases.
<222> 49-59
<223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153
 Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr
 1   5   10   15

 Gly Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe
                 20   25   30

 Asp Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly
                 35   40   45

 Leu Ala Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe
                 50   55   60

 Gln Lys His Lys Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val
                 65   70   75

 Phe Val Val Leu Ile Gly Trp Pro Leu Ile Gly Met Ile Phe Glu
                 80   85   90

 Ile Tyr Gly Phe Phe Leu Leu Phe Arg Gly Phe Phe Pro Val Val
                 95   100   105

 Val Gly Phe Ile Arg Arg Val Pro Val Leu Gly Ser Leu Leu Asn
                 110   115   120

 Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val Gly Glu Ser Asn
                 125   130   135

 Asn Met Val

<210> 154
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 66
<223> unknown base

<400> 154
 gaagacgtgg cggctctcgc ctgggctgtt tcccggcttc atttctcccg 50

 actcagcttc ccaccntggg ctttccgagg tgctttcgcc gctgtcccca 100

 ccactgcagc catgatctcc ttaacggaca cgcagaaaat tggaatggga 150

 ttaaccggat ttggagtgtt tttcctgttc tttggaatga ttctcttttt 200

 tgacaaagca ctactggcta ttggaaatgt tttatttgta gccggcttgg 250

 cttttgtaat tggtttagaa agaacattca gattcttctt ccaaaaacat 300

144

aaaatgaaag ctacaggttt ttttctgggt ggtgtatttg tagtccttat 350

tggttggcct ttgataggca tgatcttcga aatttatgga ttttttctct 400

tgttc 405

<210> 155
<211> 1781
<212> DNA
<213> Homo sapiens

<400> 155
ggcacgaggc tgaacccagc cggctccatc tcagcttctg gtttctaagt 50

ccatgtgcca aaggctgcca ggaaggagac gccttcctga gtcctggatc 100

tttcttcctt ctggaaatct ttgactgtgg gtagttattt atttctgaat 150

aagagcgtcc acgcatcatg gacctcgcgg gactgctgaa gtctcagttc 200

ctgtgccacc tggtcttctg ctacgtcttt attgcctcag ggctaatcat 250

caacaccatt cagctcttca ctctcctcct ctggcccatt aacaagcagc 300

tcttccggaa gatcaactgc agactgtcct attgcatctc aagccagctg 350

gtgatgctgc tggagtggtg gtcgggcacg gaatgcacca tcttcacgga 400

cccgcgcgcc tacctcaagt atgggaagga aaatgccatc gtggttctca 450

accacaagtt tgaaattgac tttctgtgtg gctggagcct gtccgaacgc 500

tttgggctgt taggggggctc caaggtcctg gccaagaaag agctggccta 550

tgtcccaatt atcggctgga tgtggtactt caccgagatg gtcttctgtt 600

cgcgcaagtg ggagcaggat cgcaagacgg ttgccaccag tttgcagcac 650

ctccgggact accccgagaa gtattttttc ctgattcact gtgagggcac 700

acggttcacg gagaagaagc atgagatcag catgcaggtg gcccgggcca 750

aggggctgcc tcgcctcaag catcacctgt gccacgaac caagggcttc 800

gccatcaccg tgaggagctt gagaaatgta gtttcagctg tatatgactg 850

tacactcaat ttcagaaata atgaaaatcc aacactgctg ggagtcctaa 900

acggaaagaa ataccatgca gatttgtatg ttaggaggat cccactggaa 950

gacatccctg aagacgatga cgagtgctcg gcctggctgc acaagctcta 1000

ccaggagaag gatgcctttc aggaggagta ctacaggacg ggcaccttcc 1050

cagagacgcc catggtgccc ccccggcggc cctggaccct cgtgaactgg 1100

ctgtttttggg cctcgctggt gctctaccct ttcttccagt cctggtcag 1150

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catgatcagg agcgggtctt ccctgacgct ggccagcttc atcctcgtct 1200

tctttgtggc ctccgtggga gttcgatgga tgattggtgt gacggaaatt 1250

gacaagggct ctgcctacgg caactctgac agcaagcaga aactgaatga 1300

ctgactcagg gaggtgtcac catccgaagg gaaccttggg gaactggtgg 1350

cctctgcata tcctccttag tgggacacgg tgacaaaggc tgggtgagcc 1400

cctgctgggc acggcggaag tcacgacctc ccagccagg gagtctggtc 1450

tcaaggccgg atggggagga agatgttttg taatcttttt ttccccatgt 1500

gctttagtgg gctttggttt tctttttgtg cgagtgtgtg tgagaatggc 1550

tgtgtggtga gtgtgaactt tgttctgtga tcatagaaag ggtattttag 1600

gctgcagggg agggcagggc tggggaccga aggggacaag ttcccctttc 1650

atcctttggt gctgagtttt ctgtaaccct tggttgccag agataaagtg 1700

aaaagtgctt taggtgagat gactaaatta tgcctccaag aaaaaaaaat 1750

taaagtgctt ttctgggtca aaaaaaaaaa a 1781
```

<210> 156
<211> 378
<212> PRT
<213> Homo sapiens

<400> 156
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Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu
 1               5                  10                  15

Val Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr
                20                  25                  30

Ile Gln Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu
                35                  40                  45

Phe Arg Lys Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln
                50                  55                  60

Leu Val Met Leu Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile
                65                  70                  75

Phe Thr Asp Pro Arg Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala
                80                  85                  90

Ile Val Val Leu Asn His Lys Phe Glu Ile Asp Phe Leu Cys Gly
                95                  100                 105

Trp Ser Leu Ser Glu Arg Phe Gly Leu Leu Gly Gly Ser Lys Val
                110                 115                 120

Leu Ala Lys Lys Glu Leu Ala Tyr Val Pro Ile Ile Gly Trp Met
                125                 130                 135
```
```

146
```

Trp Tyr Phe Thr Glu Met Val Phe Cys Ser Arg Lys Trp Glu Gln
                140   145   150

Asp Arg Lys Thr Val Ala Thr Ser Leu Gln His Leu Arg Asp Tyr
                155   160   165

Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu Gly Thr Arg Phe
                170   175   180

Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala Arg Ala Lys
                185   190   195

Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr Lys Gly
                200   205   210

Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala Val
                215   220   225

Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
                230   235   240

Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val
                245   250   255

Arg Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys
                260   265   270

Ser Ala Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln
                275   280   285

Glu Glu Tyr Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val
                290   295   300

Pro Pro Arg Arg Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala
                305   310   315

Ser Leu Val Leu Tyr Pro Phe Phe Gln Phe Leu Val Ser Met Ile
                320   325   330

Arg Ser Gly Ser Ser Leu Thr Leu Ala Ser Phe Ile Leu Val Phe
                335   340   345

Phe Val Ala Ser Val Gly Val Arg Trp Met Ile Gly Val Thr Glu
                350   355   360

Ile Asp Lys Gly Ser Ala Tyr Gly Asn Ser Asp Ser Lys Gln Lys
                365   370   375

Leu Asn Asp

<210> 157
<211> 1849
<212> DNA
<213> Homo sapiens

<400> 157
 ctgaggcggc ggtagcatgg aggggagag tacgtcggcg gtgctctcgg 50

147

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gctttgtgct cggcgcactc gctttccagc acctcaacac ggactcggac 100

acggaaggtt ttcttcttgg ggaagtaaaa ggtgaagcca agaacagcat 150

tactgattcc caaatggatg atgttgaagt tgtttataca attgacattc 200

agaaatatat tccatgctat cagctttta gcttttataa ttcttcaggc 250

gaagtaaatg agcaagcact gaagaaaata ttatcaaatg tcaaaaagaa 300

tgtggtaggt tggtacaaat ccgtcgtca ttcagatcag atcatgacgt 350

ttagagagag gctgcttcac aaaaacttgc aggagcattt ttcaaaccaa 400

gaccttgttt ttctgctatt aacaccaagt ataataacag aaagctgctc 450

tactcatcga ctggaacatt ccttatataa acctcaaaaa ggactttttc 500

acagggtacc tttagtggtt gccaatctgg gcatgtctga caactgggt 550

tataaaactg tatcaggttc ctgtatgtcc actggttta gccgagcagt 600

acaaacacac agctctaaat tttttgaaga agatggatcc ttaaaggagg 650

tacataagat aaatgaaatg tatgcttcat tacaagagga attaaagagt 700

atatgcaaaa aagtggaaga cagtgaacaa gcagtagata aactagtaaa 750

ggatgtaaac agattaaaac gagaaattga gaaaggaga ggagcacaga 800

ttcaggcagc aagagagaag aacatccaaa aagaccctca ggagaacatt 850

tttcttgtc aggcattacg gaccttttt ccaaattctg aatttcttca 900

ttcatgtgtt atgtctttaa aaaatagaca tgtttctaaa agtagctgta 950

actacaacca ccatctcgat gtagtagaca atctgacctt aatggtagaa 1000

cacactgaca ttcctgaagc tagtccagct agtacaccac aaatcattaa 1050

gcataaagcc ttagacttag atgacagatg gcaattcaag agatctcggt 1100

tgttagatac acaagacaaa cgatctaaag caaatactgg tagtagtaac 1150

caagataaag catccaaaat gagcagccca gaaacagatg aagaaattga 1200

aaagatgaag ggttttggtg aatattcacg gtctcctaca ttttgatcct 1250

tttaacctta caaggagatt tttttatttg gctgatgggt aaagccaaac 1300

atttctattg tttttactat gttgagctac ttgcagtaag ttcatttgtt 1350

tttactatgt tcacctgttt gcagtaatac acagataact cttagtgcat 1400

ttacttcaca aagtactttt tcaaacatca gatgctttta tttccaaacc 1450

ttttttttcac ctttcactaa gttgttgagg ggaaggctta cacagacaca 1500
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148

ttctttagaa ttggaaaagt gagaccaggc acagtggctc acacctgtaa 1550

tcccagcact tagggaagac aagtcaggag gattgattga agctaggagt 1600

tagagaccag cctgggcaac gtattgagac catgtctatt aaaaaataaa 1650

atggaaaagc aagaatagcc ttattttcaa aatatggaaa gaaatttata 1700

tgaaaattta tctgagtcat taaaattctc cttaagtgat acttttttag 1750

aagtacatta tggctagagt tgccagataa aatgctggat atcatgcaat 1800

aaatttgcaa aacatcatct aaaatttaaa aaaaaaaaa aaaaaaaa 1849

<210> 158
<211> 409
<212> PRT
<213> Homo sapiens

<400> 158

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Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu
 1               5                  10                  15

Gly Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu
                20                  25                  30

Gly Phe Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile
                35                  40                  45

Thr Asp Ser Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp
                50                  55                  60

Ile Gln Lys Tyr Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn
                65                  70                  75

Ser Ser Gly Glu Val Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser
                80                  85                  90

Asn Val Lys Lys Asn Val Val Gly Trp Tyr Lys Phe Arg Arg His
                95                  100                 105

Ser Asp Gln Ile Met Thr Phe Arg Glu Arg Leu Leu His Lys Asn
                110                 115                 120

Leu Gln Glu His Phe Ser Asn Gln Asp Leu Val Phe Leu Leu Leu
                125                 130                 135

Thr Pro Ser Ile Ile Thr Glu Ser Cys Ser Thr His Arg Leu Glu
                140                 145                 150

His Ser Leu Tyr Lys Pro Gln Lys Gly Leu Phe His Arg Val Pro
                155                 160                 165

Leu Val Val Ala Asn Leu Gly Met Ser Glu Gln Leu Gly Tyr Lys
                170                 175                 180

Thr Val Ser Gly Ser Cys Met Ser Thr Gly Phe Ser Arg Ala Val
                185                 190                 195
```

149

```
Gln Thr His Ser Ser Lys Phe Phe Glu Glu Asp Gly Ser Leu Lys
                200             205             210

Glu Val His Lys Ile Asn Glu Met Tyr Ala Ser Leu Gln Glu Glu
                215             220             225

Leu Lys Ser Ile Cys Lys Lys Val Glu Asp Ser Glu Gln Ala Val
                230             235             240

Asp Lys Leu Val Lys Asp Val Asn Arg Leu Lys Arg Glu Ile Glu
                245             250             255

Lys Arg Arg Gly Ala Gln Ile Gln Ala Ala Arg Glu Lys Asn Ile
                260             265             270

Gln Lys Asp Pro Gln Glu Asn Ile Phe Leu Cys Gln Ala Leu Arg
                275             280             285

Thr Phe Phe Pro Asn Ser Glu Phe Leu His Ser Cys Val Met Ser
                290             295             300

Leu Lys Asn Arg His Val Ser Lys Ser Ser Cys Asn Tyr Asn His
                305             310             315

His Leu Asp Val Val Asp Asn Leu Thr Leu Met Val Glu His Thr
                320             325             330

Asp Ile Pro Glu Ala Ser Pro Ala Ser Thr Pro Gln Ile Ile Lys
                335             340             345

His Lys Ala Leu Asp Leu Asp Asp Arg Trp Gln Phe Lys Arg Ser
                350             355             360

Arg Leu Leu Asp Thr Gln Asp Lys Arg Ser Lys Ala Asn Thr Gly
                365             370             375

Ser Ser Asn Gln Asp Lys Ala Ser Lys Met Ser Ser Pro Glu Thr
                380             385             390

Asp Glu Glu Ile Glu Lys Met Lys Gly Phe Gly Glu Tyr Ser Arg
                395             400             405

Ser Pro Thr Phe


<210> 159
<211> 2651
<212> DNA
<213> Homo sapiens

<400> 159
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 acgagcggac cagcgcaggg cagcccaagc agcgcgcagc gaacgcccgc 100

 cgccgcccac accctctgcg gtccccgcgg cgcctgccac ccttccctcc 150

 ttccccgcgt ccccgcctcg ccggccagtc agcttgccgg gttcgctgcc 200
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150

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ccgcgaaacc ccgaggtcac cagcccgcgc ctctgcttcc ctgggccgcg 250

cgccgcctcc acgccctcct tctcccctgg cccggcgcct ggcaccgggg 300

accgttgcct gacgcgaggc ccagctctac ttttcgcccc gcgtctcctc 350

cgcctgctcg cctcttccac caactccaac tccttctccc tccagctcca 400

ctcgctagtc cccgactccg ccagccctcg gcccgctgcc gtagcgccgc 450

ttcccgtccg gtcccaaagg tgggaacgcg tccgccccgg cccgcaccat 500

ggcacggttc ggcttgcccg cgcttctctg caccctggca gtgctcagcg 550

ccgcgctgct ggctgccgag ctcaagtcga aaagttgctc ggaagtgcga 600

cgtctttacg tgtccaaagg cttcaacaag aacgatgccc ccctccacga 650

gatcaacggt gatcatttga agatctgtcc ccagggttct acctgctgct 700

ctcaagagat ggaggagaag tacagcctgc aaagtaaaga tgatttcaaa 750

agtgtggtca gcgaacagtg caatcatttg caagctgtct ttgcttcacg 800

ttacaagaag tttgatgaat tcttcaaaga actacttgaa aatgcagaga 850

aatccctgaa tgatatgttt gtgaagacat atggccattt atacatgcaa 900

aattctgagc tatttaaaga tctcttcgta gagttgaaac gttactacgt 950

ggtgggaaat gtgaacctgg aagaaatgct aaatgacttc tgggctcgcc 1000

tcctggagcg gatgttccgc ctggtgaact cccagtacca ctttacagat 1050

gagtatctgg aatgtgtgag caagtatacg gagcagctga gcccttcgg 1100

agatgtccct cgcaaattga agctccaggt tactcgtgct tttgtagcag 1150

cccgtacttt cgctcaaggc ttagcggttg cgggagatgt cgtgagcaag 1200

gtctccgtgg taaaccccac agcccagtgt acccatgccc tgttgaagat 1250

gatctactgc tcccactgcc ggggtctcgt gactgtgaag ccatgttaca 1300

actactgctc aaacatcatg agaggctgtt tggccaacca aggggatctc 1350

gattttgaat ggaacaattt catagatgct atgctgatgg tggcagagag 1400

gctagagggt cctttcaaca ttgaatcggt catggatccc atcgatgtga 1450

agatttctga tgctattatg aacatgcagg ataatagtgt tcaagtgtct 1500

cagaaggttt tccagggatg tggacccccc aagcccctcc cagctggacg 1550

aatttctcgt tccatctctg aaagtgcctt cagtgctcgc ttcagaccac 1600

atcaccccga ggaacgccca accacagcag ctggcactag tttggaccga 1650
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151

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ctggttactg atgtcaagga gaaactgaaa caggccaaga aattctggtc 1700

ctcccttccg agcaacgttt gcaacgatga gaggatggct gcaggaaacg 1750

gcaatgagga tgactgttgg aatgggaaag gcaaaagcag gtacctgttt 1800

gcagtgacag gaaatggatt agccaaccag ggcaacaacc cagaggtcca 1850

ggttgacacc agcaaaccag acatactgat ccttcgtcaa atcatggctc 1900

ttcgagtgat gaccagcaag atgaagaatg catacaatgg gaacgacgtg 1950

gacttctttg atatcagtga tgaaagtagt ggagaaggaa gtggaagtgg 2000

ctgtgagtat cagcagtgcc cttcagagtt tgactacaat gccactgacc 2050

atgctgggaa gagtgccaat gagaaagccg acagtgctgg tgtccgtcct 2100

ggggcacagg cctacctcct cactgtcttc tgcatcttgt cctggttat 2150

gcagagagag tggagataat tctcaaactc tgagaaaaag tgttcatcaa 2200

aaagttaaaa ggcaccagtt atcacttttc taccatccta gtgactttgc 2250

tttttaaatg aatggacaac aatgtacagt ttttactatg tggccactgg 2300

tttaagaagt gctgactttg ttttctcatt cagttttggg aggaaaaggg 2350

actgtgcatt gagttggttc ctgctccccc aaaccatgtt aaacgtggct 2400

aacagtgtag gtacagaact atagttagtt gtgcatttgt gattttatca 2450

ctctattatt tgtttgtatg ttttttttctc atttcgtttg tgggtttttt 2500

tttccaactg tgatctcgcc ttgtttctta caagcaaacc agggtccctt 2550

cttggcacgt aacatgtacg tatttctgaa atattaaata gctgtacaga 2600

agcaggtttt atttatcatg ttatcttatt aaaagaaaaa gcccaaaaag 2650

c 2651
```

<210> 160
<211> 556
<212> PRT
<213> Homo sapiens

<400> 160

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Met Ala Arg Phe Gly Leu Pro Ala Leu Leu Cys Thr Leu Ala Val
 1               5                  10                  15

Leu Ser Ala Ala Leu Leu Ala Ala Glu Leu Lys Ser Lys Ser Cys
                20                  25                  30

Ser Glu Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn
                35                  40                  45

Asp Ala Pro Leu His Glu Ile Asn Gly Asp His Leu Lys Ile Cys
```

152

Pro Gln Gly Ser Thr Cys Cys Ser Gln Glu Met Glu Glu Lys Tyr
         65   70   75

Ser Leu Gln Ser Lys Asp Asp Phe Lys Ser Val Val Ser Glu Gln
         80   85   90

Cys Asn His Leu Gln Ala Val Phe Ala Ser Arg Tyr Lys Lys Phe
         95   100   105

Asp Glu Phe Phe Lys Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu
         110   115   120

Asn Asp Met Phe Val Lys Thr Tyr Gly His Leu Tyr Met Gln Asn
         125   130   135

Ser Glu Leu Phe Lys Asp Leu Phe Val Glu Leu Lys Arg Tyr Tyr
         140   145   150

Val Val Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp
         155   160   165

Ala Arg Leu Leu Glu Arg Met Phe Arg Leu Val Asn Ser Gln Tyr
         170   175   180

His Phe Thr Asp Glu Tyr Leu Glu Cys Val Ser Lys Tyr Thr Glu
         185   190   195

Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Leu Gln
         200   205   210

Val Thr Arg Ala Phe Val Ala Ala Arg Thr Phe Ala Gln Gly Leu
         215   220   225

Ala Val Ala Gly Asp Val Val Ser Lys Val Ser Val Val Asn Pro
         230   235   240

Thr Ala Gln Cys Thr His Ala Leu Leu Lys Met Ile Tyr Cys Ser
         245   250   255

His Cys Arg Gly Leu Val Thr Val Lys Pro Cys Tyr Asn Tyr Cys
         260   265   270

Ser Asn Ile Met Arg Gly Cys Leu Ala Asn Gln Gly Asp Leu Asp
         275   280   285

Phe Glu Trp Asn Asn Phe Ile Asp Ala Met Leu Met Val Ala Glu
         290   295   300

Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile
         305   310   315

Asp Val Lys Ile Ser Asp Ala Ile Met Asn Met Gln Asp Asn Ser
         320   325   330

Val Gln Val Ser Gln Lys Val Phe Gln Gly Cys Gly Pro Pro Lys
         335   340   345

Pro Leu Pro Ala Gly Arg Ile Ser Arg Ser Ile Ser Glu Ser Ala
                350   355   360

Phe Ser Ala Arg Phe Arg Pro His His Pro Glu Glu Arg Pro Thr
                365   370   375

Thr Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Val Lys
                380   385   390

Glu Lys Leu Lys Gln Ala Lys Lys Phe Trp Ser Ser Leu Pro Ser
                395   400   405

Asn Val Cys Asn Asp Glu Arg Met Ala Ala Gly Asn Gly Asn Glu
                410   415   420

Asp Asp Cys Trp Asn Gly Lys Gly Lys Ser Arg Tyr Leu Phe Ala
                425   430   435

Val Thr Gly Asn Gly Leu Ala Asn Gln Gly Asn Asn Pro Glu Val
                440   445   450

Gln Val Asp Thr Ser Lys Pro Asp Ile Leu Ile Leu Arg Gln Ile
                455   460   465

Met Ala Leu Arg Val Met Thr Ser Lys Met Lys Asn Ala Tyr Asn
                470   475   480

Gly Asn Asp Val Asp Phe Phe Asp Ile Ser Asp Glu Ser Ser Gly
                485   490   495

Glu Gly Ser Gly Ser Gly Cys Glu Tyr Gln Gln Cys Pro Ser Glu
                500   505   510

Phe Asp Tyr Asn Ala Thr Asp His Ala Gly Lys Ser Ala Asn Glu
                515   520   525

Lys Ala Asp Ser Ala Gly Val Arg Pro Gly Ala Gln Ala Tyr Leu
                530   535   540

Leu Thr Val Phe Cys Ile Leu Phe Leu Val Met Gln Arg Glu Trp
                545   550   555

Arg

<210> 161
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 161
 ctccgtggta aaccccacag ccc 23

<210> 162
<211> 24

154

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 162
 tcacatcgat gggatccatg accg 24

<210> 163
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 163
 ggtctcgtga ctgtgaagcc atgttacaac tactgctcaa acatcatgag 50

<210> 164
<211> 870
<212> DNA
<213> Homo sapiens

<400> 164
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 gctgagtatc ctgacctgag tcatccccag ggatcaggag cctccagcag 100

 ggaaccttcc attatattct tcaagcaact tacagctgca ccgacagttg 150

 cgatgaaagt tctaatctct tccctcctcc tgttgctgcc actaatgctg 200

 atgtccatgg tctctagcag cctgaatcca ggggtcgcca gaggccacag 250

 ggaccgaggc caggcttcta ggagatggct ccaggaaggc ggccaagaat 300

 gtgagtgcaa agattggttc ctgagagccc cgagaagaaa attcatgaca 350

 gtgtctgggc tgccaaagaa gcagtgcccc tgtgatcatt tcaagggcaa 400

 tgtgaagaaa acaagacacc aaaggcacca cagaaagcca aacaagcatt 450

 ccagagcctg ccagcaattt ctcaaacaat gtcagctaag aagctttgct 500

 ctgcctttgt aggagctctg agcgcccact cttccaatta aacattctca 550

 gccaagaaga cagtgagcac acctaccaga cactcttctt ctcccacctc 600

 actctcccac tgtacccacc cctaaatcat tccagtgctc tcaaaaagca 650

 tgttttttcaa gatcattttg tttgttgctc tctctagtgt cttcttctct 700

 cgtcagtctt agcctgtgcc ctccccttac ccaggcttag gcttaattac 750

 ctgaaagatt ccaggaaact gtagcttcct agctagtgtc atttaacctt 800

155

aaatgcaatc aggaaagtag caaacagaag tcaataaata tttttaaatg 850

tcaaaaaaaa aaaaaaaaa 870

<210> 165
<211> 119
<212> PRT
<213> Homo sapiens

<400> 165
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met
 1   5   10   15

Leu Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg
                20   25   30

Gly His Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu
                35   40   45

Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro
                50   55   60

Arg Arg Lys Phe Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys
                65   70   75

Pro Cys Asp His Phe Lys Gly Asn Val Lys Lys Thr Arg His Gln
                80   85   90

Arg His His Arg Lys Pro Asn Lys His Ser Arg Ala Cys Gln Gln
                95   100   105

Phe Leu Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro Leu
                110   115

<210> 166
<211> 551
<212> DNA
<213> Homo sapiens

<400> 166
aatggctgtc ttagtacttc gcctgacagt tgtcctggga ctgcttgtct 50

tattcctgac ctgctatgca gacgacaaac cagacaagcc agacgacaag 100

ccagacgact cgggcaaaga cccaaagcca gacttcccca aattcctaag 150

cctcctgggc acagagatca ttgagaatgc agtcgagttc atcctccgct 200

ccatgtccag gagcacagga tttatggaat ttgatgataa tgaaggaaaa 250

cattcatcaa agtgacatcc tcaggacaca cccatgtggc tcctggacaa 300

tccaagagca gccaaatcct gcttttccag tttggctcca caagtcctcc 350

aggacagagc cctcaaagca actcccaacg agttctcagg attcaggctc 400

tggcttcaac caaacagaac tcattttgaa caccctgact gcattttgc 450

156

ttttagaaag ttagaataaa tatggcgctt tgggatcaca tagttgatgg 500

agaggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550

a 551

<210> 167
<211> 87
<212> PRT
<213> Homo sapiens

<400> 167
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Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu
 1               5                  10                  15

Val Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro
                20                  25                  30

Asp Asp Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe
                35                  40                  45

Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala
                50                  55                  60

Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met
                65                  70                  75

Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys
                80                  85
```

<210> 168
<211> 1371
<212> DNA
<213> Homo sapiens

<400> 168
ggacgccagc gcctgcagag gctgagcagg gaaaaagcca gtgccccagc 50

ggaagcacag ctcagagctg gtctgccatg gacatcctgg tcccactcct 100

gcagctgctg gtgctgcttc ttaccctgcc cctgcacctc atggctctgc 150

tgggctgctg gcagcccctg tgcaaaagct acttcccta cctgatggcc 200

gtgctgactc ccaagagcaa ccgcaagatg gagagcaaga acgggagct 250

cttcagccag ataaagggc ttacaggagc ctccgggaaa gtggccctac 300

tggagctggg ctgcggaacc ggagccaact ttcagttcta cccaccgggc 350

tgcagggtca cctgcctaga cccaaatccc cactttgaga agttcctgac 400

aaagagcatg gctgagaaca ggcacctcca atatgagcgg tttgtggtgg 450

ctcctggaga ggacatgaga cagctggctg atggctccat ggatgtggtg 500

gtctgcactc tggtgctgtg ctctgtgcag agcccaagga aggtcctgca 550

157

ggaggtccgg agagtactga gaccgggagg tgtgctcttt ttctgggagc 600

atgtggcaga accatatgga agctgggcct tcatgtggca gcaagttttc 650

gagcccacct ggaaacacat tggggatggc tgctgcctca ccagagagac 700

ctggaaggat cttgagaacg cccagttctc cgaaatccaa atggaacgac 750

agccccctcc cttgaagtgg ctacctgttg ggccccacat catgggaaag 800

gctgtcaaac aatctttccc aagctccaag gcactcattt gctccttccc 850

cagcctccaa ttagaacaag ccacccacca gcctatctat cttccactga 900

gagggaccta gcagaatgag agaagacatt catgtaccac ctactagtcc 950

ctctctcccc aacctctgcc agggcaatct ctaacttcaa tcccgccttc 1000

gacagtgaaa aagctctact tctacgctga cccagggagg aaacactagg 1050

accctgttgt atcctcaact gcaagtttct ggactagtct cccaacgttt 1100

gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gctcctctcg 1150

ctttcctcct gaggctacac ccatgcgtct ctaggaactg gtcacaaaag 1200

tcatggtgcc tgcatccctg ccaagccccc ctgaccctct ctccccacta 1250

ccaccttctt cctgagctgg gggcaccagg gagaatcaga gatgctgggg 1300

atgccagagc aagactcaaa gaggcagagg ttttgttctc aaatattttt 1350

taataaatag acgaaaccac g 1371

<210> 169
<211> 277
<212> PRT
<213> Homo sapiens

<400> 169
Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu
 1   5   10   15

Thr Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro
             20   25   30

Leu Cys Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro
                 35   40   45

Lys Ser Asn Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser
             50   55   60

Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu
             65   70   75

Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro
             80   85   90

158

Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His Phe Glu Lys
                95   100   105

Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln Tyr Glu
                110   115   120

Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala Asp
                125   130   135

Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val
                140   145   150

Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg
                155   160   165

Pro Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr
                170   175   180

Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp
                185   190   195

Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys
                200   205   210

Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln
                215   220   225

Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
                230   235   240

Lys Ala Val Lys Gln Ser Phe Pro Ser Ser Lys Ala Leu Ile Cys
                245   250   255

Ser Phe Pro Ser Leu Gln Leu Glu Gln Ala Thr His Gln Pro Ile
                260   265   270

Tyr Leu Pro Leu Arg Gly Thr
                275

<210> 170
<211> 1621
<212> DNA
<213> Homo sapiens

<400> 170
gtgggattta tttgagtgca agatcgtttt ctcagtggtg gtggaagttg 50

cctcatcgca ggcagatgtt ggggctttgt ccgaacagct cccctctgcc 100

agcttctgta gataagggtt aaaaactaat atttatatga cagaagaaaa 150

agatgtcatt ccgtaaagta aacatcatca tcttggtcct ggctgttgct 200

ctcttcttac tggttttgca ccataacttc ctcagcttga gcagtttgtt 250

aaggaatgag gttacagatt caggaattgt agggcctcaa cctatagact 300

ttgtcccaaa tgctctccga catgcagtag atgggagaca agaggagatt 350

159

cctgtggtca tcgctgcatc tgaagacagg cttgggggg ccattgcagc 400

tataaacagc attcagcaca acactcgctc caatgtgatt ttctacattg 450

ttactctcaa caatacagca gaccatctcc ggtcctggct caacagtgat 500

tccctgaaaa gcatcagata caaaattgtc aattttgacc ctaaactttt 550

ggaaggaaaa gtaaaggagg atcctgacca gggggaatcc atgaaacctt 600

taacctttgc aaggttctac ttgccaattc tggttcccag cgcaaagaag 650

gccatataca tggatgatga tgtaattgtg caaggtgata ttcttgccct 700

ttacaataca gcactgaagc caggacatgc agctgcattt tcagaagatt 750

gtgattcagc ctctactaaa gttgtcatcc gtggagcagg aaaccagtac 800

aattacattg gctatcttga ctataaaaag gaaagaattc gtaagctttc 850

catgaaagcc agcacttgct catttaatcc tggagttttt gttgcaaacc 900

tgacggaatg gaaacgacag aatataacta accaactgga aaaatggatg 950

aaactcaatg tagaagaggg actgtatagc agaaccctgg ctggtagcat 1000

cacaacacct cctctgctta tcgtatttta tcaacagcac tctaccatcg 1050

atcctatgtg gaatgtccgc caccttggtt ccagtgctgg aaaacgatat 1100

tcacctcagt ttgtaaaggc tgccaagtta ctccattgga atggacattt 1150

gaagccatgg ggaaggactg cttcatatac tgatgtttgg gaaaaatggt 1200

atattccaga cccaacaggc aaattcaacc taatccgaag atataccgag 1250

atctcaaaca taaagtgaaa cagaatttga actgtaagca agcatttctc 1300

aggaagtcct ggaagatagc atgcatggga agtaacagtt gctaggcttc 1350

aatgcctatc ggtagcaagc catggaaaaa gatgtgtcag ctaggtaaag 1400

atgacaaact gccctgtctg gcagtcagct tcccagacag actatagact 1450

ataaatatgt ctccatctgc cttaccaagt gttttcttac tacaatgctg 1500

aatgactgga aagaagaact gatatggcta gttcagctag ctggtacaga 1550

taattcaaaa ctgctgttgg ttttaatttt gtaacctgtg gcctgatctg 1600

taaataaaac ttacattttt c 1621

<210> 171
<211> 371
<212> PRT
<213> Homo sapiens

<400> 171

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Met Ser Phe Arg Lys Val Asn Ile Ile Ile Leu Val Leu Ala Val
1               5                   10              15

Ala Leu Phe Leu Leu Val Leu His His Asn Phe Leu Ser Leu Ser
                20                  25              30

Ser Leu Leu Arg Asn Glu Val Thr Asp Ser Gly Ile Val Gly Pro
                35                  40              45

Gln Pro Ile Asp Phe Val Pro Asn Ala Leu Arg His Ala Val Asp
                50                  55              60

Gly Arg Gln Glu Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp
                65                  70              75

Arg Leu Gly Gly Ala Ile Ala Ala Ile Asn Ser Ile Gln His Asn
                80                  85              90

Thr Arg Ser Asn Val Ile Phe Tyr Ile Val Thr Leu Asn Asn Thr
                95                  100             105

Ala Asp His Leu Arg Ser Trp Leu Asn Ser Asp Ser Leu Lys Ser
                110                 115             120

Ile Arg Tyr Lys Ile Val Asn Phe Asp Pro Lys Leu Leu Glu Gly
                125                 130             135

Lys Val Lys Glu Asp Pro Asp Gln Gly Glu Ser Met Lys Pro Leu
                140                 145             150

Thr Phe Ala Arg Phe Tyr Leu Pro Ile Leu Val Pro Ser Ala Lys
                155                 160             165

Lys Ala Ile Tyr Met Asp Asp Asp Val Ile Val Gln Gly Asp Ile
                170                 175             180

Leu Ala Leu Tyr Asn Thr Ala Leu Lys Pro Gly His Ala Ala Ala
                185                 190             195

Phe Ser Glu Asp Cys Asp Ser Ala Ser Thr Lys Val Val Ile Arg
                200                 205             210

Gly Ala Gly Asn Gln Tyr Asn Tyr Ile Gly Tyr Leu Asp Tyr Lys
                215                 220             225

Lys Glu Arg Ile Arg Lys Leu Ser Met Lys Ala Ser Thr Cys Ser
                230                 235             240

Phe Asn Pro Gly Val Phe Val Ala Asn Leu Thr Glu Trp Lys Arg
                245                 250             255

Gln Asn Ile Thr Asn Gln Leu Glu Lys Trp Met Lys Leu Asn Val
                260                 265             270

Glu Glu Gly Leu Tyr Ser Arg Thr Leu Ala Gly Ser Ile Thr Thr
                275                 280             285

Pro Pro Leu Leu Ile Val Phe Tyr Gln Gln His Ser Thr Ile Asp
```

161

```
                290                 295                 300

    Pro Met Trp Asn Val Arg His Leu Gly Ser Ser Ala Gly Lys Arg
                    305                 310                 315

    Tyr Ser Pro Gln Phe Val Lys Ala Ala Lys Leu Leu His Trp Asn
                    320                 325                 330

    Gly His Leu Lys Pro Trp Gly Arg Thr Ala Ser Tyr Thr Asp Val
                    335                 340                 345

    Trp Glu Lys Trp Tyr Ile Pro Asp Pro Thr Gly Lys Phe Asn Leu
                    350                 355                 360

    Ile Arg Arg Tyr Thr Glu Ile Ser Asn Ile Lys
                    365                 370
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<210> 172
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 71, 76, 86, 91, 162, 220, 269, 281
<223> unknown base

<400> 172

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 aggttacaga ttcaggaatt ntaggncctc aacctntaga ntttgtccca 100

 aatgttctcc gacatgcagt agatgggaga caagaggaga ttcctgtggt 150

 catcgctgca tntgaagaca ggcttggggg ggccattgca gctataaaca 200

 gcattcagca caacactcgn tccaatgtga ttttctacat tgttactctc 250

 aacaatacag cagaccatnt ccggtcctgg ntcaacagtg attccctgaa 300

 aagcatcaga tacaaaattg tcaattttga ccctaaactt ttggaaggaa 350

 aagtaaagga ggatcctgac caggggaat ccatgaaacc tttaaccttt 400

 gcaaggttct acttgccaat tctggttccc agcgcaaaga aggccatata 450

 catggatgat gatgtaattg tgcaaggtga tattcttgcc ctttacaata 500

 cagcactgaa gccaggacat gcagctgcat tttcagaaga ttgtgattca 550

 gcctctacta aagttgtcat ccgtggagca ggaaa 585
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<210> 173
<211> 1866
<212> DNA
<213> Homo sapiens

<400> 173

162

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cgacgctcta gcggttaccg ctgcgggctg gctgggcgta gtggggctgc 50

gcggctgcca cggagctaga gggcaagtgt gctcggccca gcgtgcaggg 100

aacgcgggcg gccagacaac gggctgggct ccggggcctg cggcgcgggc 150

gctgagctgg cagggcgggt cggggcgcgg gctgcatccg catctcctcc 200

atcgcctgca gtaagggcgg ccgcggcgag cctttgaggg gaacgacttg 250

tcggagccct aaccaggggt gtctctgagc ctggtgggat ccccggagcg 300

tcacatcact ttccgatcac ttcaaagtgg ttaaaaacta atatttatat 350

gacagaagaa aaagatgtca ttccgtaaag taaacatcat catcttggtc 400

ctgggctgtt gctctcttct tactggtttt gcaccataac ttcctcagct 450

tgaggcagtt tgttaaggaa tgaggttaca gattcaggaa ttgtagggcc 500

tcaacctata ggactttgtc ccaaatgctc tccgacatgc agtagatggg 550

agacaagagg agattcctgt ggtcatcgct gcatctgaag acaggcttgg 600

gggggccatt gcagctataa acagcattca gcacaacact cgctccaatg 650

tgattttcta cattgttact ctcaacaata cagcagacca tctccggtcc 700

tgggctcaac agtgattccc tgaaaagcat cagatacaaa attgtcaatt 750

ttgaccctaa acttttggaa ggaaaagtaa aggaggatcc tgaccagggg 800

gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctggg 850

ttcccagcgc aaagaaggcc atatacatgg atgatgatgt aattgtgcaa 900

ggtgatattc ttgccctttta caatacagca ctgaagccag acatgcagc 950

tgcattttca gaagattgtg attcagcctc tactaaagtt gtcatccgtg 1000

gagcaggaaa ccagtacaat tacattggct atcttgacta taaaaaggaa 1050

agaattcgta agctttccat gaaagccagc acttgctcat ttaatcctgg 1100

agtttttgtt gcaaacctga cggaatggaa acgacagaat ataactaacc 1150

aactggaaaa atggatgaaa ctcaatgtag aagagggact gtatagcaga 1200

accctggctg gtagcatcac aacacctcct ctgcttatcg tattttatca 1250

acagcactct accatcgatc ctatgtggaa tgtccgccac cttggttcca 1300

gtgctggaaa acgatattca cctcagtttg taaaggctgc caagttactc 1350

cattggaatg gacatttgaa gccatgggga aggactgctt catatactga 1400

tgtttgggga aaaatggtat attccagacc caacaggcaa attcaaccta 1450
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163

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atccgaagat ataccgagat ctcaaacata aagtgaaaca gaatttgaac 1500

tgtaagcaag catttctcag gaagtcctgg aagatagcat gcgtgggaag 1550

taacagttgc taggcttcaa tgcctatcgg tagcaagcca tggaaaaaga 1600

tgtgtcagct aggtaaagat gacaaactgc cctgtctggc agtcagcttc 1650

ccagacagac tatagactat aaatatgtct ccatctgcct taccaagtgt 1700

tttcttacta caatgctgaa tgactggaaa gaagaactga tatggctagt 1750

tcagctagct ggtacagata attcaaaact gctgttggtt ttaattttgt 1800

aacctgtggc ctgatctgta aataaaactt acatttttca ataggtaaaa 1850

aaaaaaaaa aaaaaa 1866
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<210> 174
<211> 823
<212> DNA
<213> Homo sapiens

<400> 174
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ctcaccattg aggcagctcc actgtctgtg ctggtctgag ggtgctgcct 150

gtcatggggg cagccatctc ccaggggggcc ctcatcgcca tcgtctgcaa 200

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agccatgaag gcagctacct gctgcagccc tgaaggcccc tggcctagcc 400

tggagcccag gacctaagtc cacctcacct agagcctgga attaggatcc 450

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gagccagggc catctggact atgctccatc ccaagggcca agggtcaggg 650

gccgggtcca ctctttccct aggctgagca cctctaggcc ctctaggttg 700

gggaagcaaa ctggaaccca tggcaataat aggagggtgt ccaggctggg 750

cccctcccct ggtcctccca gtgtttgctg gataataaat ggaactatgg 800

ctctaaaaaa aaaaaaaaaa aaa 823
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164

<210> 175
<211> 87
<212> PRT
<213> Homo sapiens

<400> 175
Met Gly Ala Ala Ile Ser Gln Gly Ala Leu Ile Ala Ile Val Cys
1   5   10   15

Asn Gly Leu Val Gly Phe Leu Leu Leu Leu Leu Trp Val Ile Leu
                20   25   30

Cys Trp Ala Cys His Ser Arg Leu Pro Thr Leu Thr Leu Ser Leu
                35   40   45

Asn Pro Val Pro Thr Pro Ala Leu Ala Pro Val Leu Arg Arg Pro
                50   55   60

His His Pro Arg Ser Pro Ala Met Lys Ala Ala Thr Cys Cys Ser
                65   70   75

Pro Glu Gly Pro Trp Pro Ser Leu Glu Pro Arg Thr
                80   85

<210> 176
<211> 1660
<212> DNA
<213> Homo sapiens

<400> 176
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tgtccctcaa acacctgagt gctactccct atttgcatct gttttgataa 150

atgatgttga caccctccac cgaattctaa gtggaatcat gtcgggaaga 200

gatacaatcc ttggcctgtg tatcctcgca ttagccttgt ctttggccat 250

gatgtttacc ttcagattca tcaccaccct tctggttcac attttcattt 300

cattggttat tttgggattg ttgtttgtct gcggtgtttt atggtggctg 350

tattatgact ataccaacga cctcagcata gaattggaca cagaaaggga 400

aaatatgaag tgcgtgctgg ggtttgctat cgtatccaca ggcatcacgg 450

cagtgctgct cgtcttgatt tttgttctca gaaagagaat aaaattgaca 500

gttgagcttt tccaaatcac aaataaagcc atcagcagtg ctcccttcct 550

gctgttccag ccactgtgga catttgccat cctcattttc ttctgggtcc 600

tctgggtggc tgtgctgctg agcctgggaa ctgcaggagc tgcccaggtt 650

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165

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cgtgccagca aatgactata gctggggcag tggttacttg ttatttcaac 800

agaagtaaaa atgatcctcc tgatcatccc atcctttcgt ctctctccat 850

tctcttcttc taccatcaag gaaccgttgt gaaagggtca tttttaatct 900

ctgtggtgag gattccgaga atcattgtca tgtacatgca aaacgcactg 950

aaagaacagc agcatggtgc attgtccagg tacctgttcc gatgctgcta 1000

ctgctgtttc tggtgtcttg acaaatacct gctccatctc aaccagaatg 1050

catatactac aactgctatt aatgggacag atttctgtac atcagcaaaa 1100

gatgcattca aaatcttgtc caagaactca agtcacttta catctattaa 1150

ctgctttgga gacttcataa tttttctagg aaaggtgtta gtggtgtgtt 1200

tcactgtttt tggaggactc atggctttta actacaatcg ggcattccag 1250

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ccatagtttt ttatctgtgt ttgaaactgt gctggatgca cttttcctgt 1350

gttttgctgt tgatctggaa acaaatgatg gatcgtcaga aaagccctac 1400

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caatgcaagg gcacagcagg acaagcactc attaaggaat gaggagggaa 1500

cagaactcca ggccattgtg agatagatac ccatttaggt atctgtacct 1550

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<210> 177
<211> 445
<212> PRT
<213> Homo sapiens

<400> 177
Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu
1   5   10   15

Ala Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr
                20   25   30

Leu Leu Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu
                35   40   45

Phe Val Cys Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn
                50   55   60

166

Asp Leu Ser Ile Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys
            65   70   75

Val Leu Gly Phe Ala Ile Val Ser Thr Gly Ile Thr Ala Val Leu
            80   85   90

Leu Val Leu Ile Phe Val Leu Arg Lys Arg Ile Lys Leu Thr Val
            95   100   105

Glu Leu Phe Gln Ile Thr Asn Lys Ala Ile Ser Ser Ala Pro Phe
            110   115   120

Leu Leu Phe Gln Pro Leu Trp Thr Phe Ala Ile Leu Ile Phe Phe
            125   130   135

Trp Val Leu Trp Val Ala Val Leu Leu Ser Leu Gly Thr Ala Gly
            140   145   150

Ala Ala Gln Val Met Glu Gly Gly Gln Val Glu Tyr Lys Pro Leu
            155   160   165

Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu Ile Gly Leu Ile
            170   175   180

Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met Thr Ile Ala
            185   190   195

Gly Ala Val Val Thr Cys Tyr Phe Asn Arg Ser Lys Asn Asp Pro
            200   205   210

Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe Tyr
            215   220   225

His Gln Gly Thr Val Val Lys Gly Ser Phe Leu Ile Ser Val Val
            230   235   240

Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys
            245   250   255

Glu Gln Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys
            260   265   270

Tyr Cys Cys Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn
            275   280   285

Gln Asn Ala Tyr Thr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys
            290   295   300

Thr Ser Ala Lys Asp Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser
            305   310   315

His Phe Thr Ser Ile Asn Cys Phe Gly Asp Phe Ile Ile Phe Leu
            320   325   330

Gly Lys Val Leu Val Val Cys Phe Thr Val Phe Gly Gly Leu Met
            335   340   345

Ala Phe Asn Tyr Asn Arg Ala Phe Gln Val Trp Ala Val Pro Leu

167

Leu Leu Val Ala Phe Phe Ala Tyr Leu Val Ala His Ser Phe Leu
            365   370   375

Ser Val Phe Glu Thr Val Leu Asp Ala Leu Phe Leu Cys Phe Ala
            380   385   390

Val Asp Leu Glu Thr Asn Asp Gly Ser Ser Glu Lys Pro Tyr Phe
            395   400   405

Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser Asn Lys Leu
            410   415   420

Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg Asn Glu
            425   430   435

Glu Gly Thr Glu Leu Gln Ala Ile Val Arg
            440   445

<210> 178
<211> 2773
<212> DNA
<213> Homo sapiens

<400> 178
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 aagggaaaaa gaatattcat tctgtgtggt gaaaattttt tgaaaaaaaa 150

 attgccttct tcaaacaagg gtgtcattct gatatttatg aggactgttg 200

 ttctcactat gaaggcatct gttattgaaa tgttccttgt tttgctggtg 250

 actggagtac attcaaacaa agaaacggca aagaagatta aaaggcccaa 300

 gttcactgtg cctcagatca actgcgatgt caaagccgga aagatcatcg 350

 atcctgagtt cattgtgaaa tgtccagcag gatgccaaga ccccaaatac 400

 catgtttatg gcactgacgt gtatgcatcc tactccagtg tgtgtggcgc 450

 tgccgtacac agtggtgtgc ttgataattc aggagggaaa atacttgttc 500

 ggaaggttgc tggacagtct ggttacaaag ggagttattc caacggtgtc 550

 caatcgttat ccctaccacg atggagagaa tcctttatcg tcttagaaag 600

 taaacccaaa aagggtgtaa cctacccatc agctcttaca tactcatcat 650

 cgaaaagtcc agctgcccaa gcaggtgaga ccacaaaagc ctatcagagg 700

 ccacctattc cagggacaac tgcacagccg gtcactctga tgcagcttct 750

 ggctgtcact gtagctgtgg ccaccCCCAC cacCTTGCCA aggccatccc 800

cttctgctgc ttctaccacc agcatcccca gaccacaatc agtgggccac 850

aggagccagg agatggatct ctggtccact gccacctaca caagcagcca 900

aaacaggccc agagctgatc caggtatcca aaggcaagat ccttcaggag 950

ctgccttcca gaaacctgtt ggagcggatg tcagcctggg acttgttcca 1000

aaagaagaat tgagcacaca gtctttggag ccagtatccc tgggagatcc 1050

aaactgcaaa attgacttgt cgtttttaat tgatgggagc accagcattg 1100

gcaaacggcg attccgaatc cagaagcagc tcctggctga tgttgcccaa 1150

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tggaaacaga agcggggctc ccaatgtggt ggtggtgatg gtggatggct 1400

ggcccacgga caaagtggag gaggcttcaa gacttgcgag agagtcagga 1450

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gcttctactc gctccacgtg cagagctggt ttggcctcca caagaccctg 1600

cagcctctgg tgaagcgggt ctgcgacact gaccgcctgg cctgcagcaa 1650

gacctgcttg aactcggctg acattggctt cgtcatcgac ggctccagca 1700

gtgtggggac gggcaacttc cgcaccgtcc tccagtttgt gaccaacctc 1750

accaaagagt ttgagatttc cgacacggac acgcgcatcg gggccgtgca 1800

gtacacctac gaacagcggc tggagtttgg gttcgacaag tacagcagca 1850

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gtccaagccc aacaagagga agttaatgat cctcatcacc gacgggaggt 2000

cctacgacga cgtccggatc ccagccatgg ctgcccatct gaagggagtg 2050

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ttcaactcac agcctcggaa ctgaattcag agcaggcaga gcaccagcaa 2250

169

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gaatacagtg cagcccttac gacaggctta cgtagagctt ttgtgagatt 2550

tttaagttgt tatttctgat ttgaactctg taaccctcag caagtttcat 2600

ttttgtcatg acaatgtagg aattgctgaa ttaaatgttt agaaggatga 2650

aaaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2750

aaaaaaaaaa aaaaaaaaaa aag 2773
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<210> 179
<211> 678
<212> PRT
<213> Homo sapiens

<400> 179

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Met Arg Thr Val Val Leu Thr Met Lys Ala Ser Val Ile Glu Met
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Phe Leu Val Leu Leu Val Thr Gly Val His Ser Asn Lys Glu Thr
                 20                  25                  30

Ala Lys Lys Ile Lys Arg Pro Lys Phe Thr Val Pro Gln Ile Asn
                 35                  40                  45

Cys Asp Val Lys Ala Gly Lys Ile Ile Asp Pro Glu Phe Ile Val
                 50                  55                  60

Lys Cys Pro Ala Gly Cys Gln Asp Pro Lys Tyr His Val Tyr Gly
                 65                  70                  75

Thr Asp Val Tyr Ala Ser Tyr Ser Ser Val Cys Gly Ala Ala Val
                 80                  85                  90

His Ser Gly Val Leu Asp Asn Ser Gly Gly Lys Ile Leu Val Arg
                 95                  100                 105

Lys Val Ala Gly Gln Ser Gly Tyr Lys Gly Ser Tyr Ser Asn Gly
                 110                 115                 120

Val Gln Ser Leu Ser Leu Pro Arg Trp Arg Glu Ser Phe Ile Val
                 125                 130                 135

Leu Glu Ser Lys Pro Lys Lys Gly Val Thr Tyr Pro Ser Ala Leu
                 140                 145                 150
```

170

Thr Tyr Ser Ser Ser Lys Ser Pro Ala Ala Gln Ala Gly Glu Thr
                155   160   165

Thr Lys Ala Tyr Gln Arg Pro Pro Ile Pro Gly Thr Thr Ala Gln
                170   175   180

Pro Val Thr Leu Met Gln Leu Leu Ala Val Thr Val Ala Val Ala
                185   190   195

Thr Pro Thr Thr Leu Pro Arg Pro Ser Pro Ser Ala Ala Ser Thr
                200   205   210

Thr Ser Ile Pro Arg Pro Gln Ser Val Gly His Arg Ser Gln Glu
                215   220   225

Met Asp Leu Trp Ser Thr Ala Thr Tyr Thr Ser Ser Gln Asn Arg
                230   235   240

Pro Arg Ala Asp Pro Gly Ile Gln Arg Gln Asp Pro Ser Gly Ala
                245   250   255

Ala Phe Gln Lys Pro Val Gly Ala Asp Val Ser Leu Gly Leu Val
                260   265   270

Pro Lys Glu Glu Leu Ser Thr Gln Ser Leu Glu Pro Val Ser Leu
                275   280   285

Gly Asp Pro Asn Cys Lys Ile Asp Leu Ser Phe Leu Ile Asp Gly
                290   295   300

Ser Thr Ser Ile Gly Lys Arg Arg Phe Arg Ile Gln Lys Gln Leu
                305   310   315

Leu Ala Asp Val Ala Gln Ala Leu Asp Ile Gly Pro Ala Gly Pro
                320   325   330

Leu Met Gly Val Val Gln Tyr Gly Asp Asn Pro Ala Thr His Phe
                335   340   345

Asn Leu Lys Thr His Thr Asn Ser Arg Asp Leu Lys Thr Ala Ile
                350   355   360

Glu Lys Ile Thr Gln Arg Gly Gly Leu Ser Asn Val Gly Arg Ala
                365   370   375

Ile Ser Phe Val Thr Lys Asn Phe Phe Ser Lys Ala Asn Gly Asn
                380   385   390

Arg Ser Gly Ala Pro Asn Val Val Val Met Val Asp Gly Trp
                395   400   405

Pro Thr Asp Lys Val Glu Glu Ala Ser Arg Leu Ala Arg Glu Ser
                410   415   420

Gly Ile Asn Ile Phe Phe Ile Thr Ile Glu Gly Ala Ala Glu Asn
                425   430   435

Glu Lys Gln Tyr Val Val Glu Pro Asn Phe Ala Asn Lys Ala Val

171

Cys Arg Thr Asn Gly Phe Tyr Ser Leu His Val Gln Ser Trp Phe
                455   460   465

Gly Leu His Lys Thr Leu Gln Pro Leu Val Lys Arg Val Cys Asp
                470   475   480

Thr Asp Arg Leu Ala Cys Ser Lys Thr Cys Leu Asn Ser Ala Asp
                485   490   495

Ile Gly Phe Val Ile Asp Gly Ser Ser Val Gly Thr Gly Asn
                500   505   510

Phe Arg Thr Val Leu Gln Phe Val Thr Asn Leu Thr Lys Glu Phe
                515   520   525

Glu Ile Ser Asp Thr Asp Thr Arg Ile Gly Ala Val Gln Tyr Thr
                530   535   540

Tyr Glu Gln Arg Leu Glu Phe Gly Phe Asp Lys Tyr Ser Ser Lys
                545   550   555

Pro Asp Ile Leu Asn Ala Ile Lys Arg Val Gly Tyr Trp Ser Gly
                560   565   570

Gly Thr Ser Thr Gly Ala Ala Ile Asn Phe Ala Leu Glu Gln Leu
                575   580   585

Phe Lys Lys Ser Lys Pro Asn Lys Arg Lys Leu Met Ile Leu Ile
                590   595   600

Thr Asp Gly Arg Ser Tyr Asp Asp Val Arg Ile Pro Ala Met Ala
                605   610   615

Ala His Leu Lys Gly Val Ile Thr Tyr Ala Ile Gly Val Ala Trp
                620   625   630

Ala Ala Gln Glu Glu Leu Glu Val Ile Ala Thr His Pro Ala Arg
                635   640   645

Asp His Ser Phe Phe Val Asp Glu Phe Asp Asn Leu His Gln Tyr
                650   655   660

Val Pro Arg Ile Ile Gln Asn Ile Cys Thr Glu Phe Asn Ser Gln
                665   670   675

Pro Arg Asn

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gcaggcatcg gggctggcgt ggactcctac tttgagtact tggtgaaagg 750

agccatcctg cttcaggata agaagctcat ggccatgttc ctagagtata 800

acaaagccat ccggaactac acccgcttcg atgactggta cctgtgggtt 850

cagatgtaca aggggactgt gtccatgcca gtcttccagt ccttggaggc 900

ctactggcct ggtcttcaga gcctcattgg agacattgac aatgccatga 950

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gaattctaca acattcctca gggatacaca gtggagaagc gagagggcta 1050

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173

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<210> 181
<211> 541
<212> PRT
<213> Homo sapiens

<400> 181
Met Pro Phe Arg Leu Leu Ile Pro Leu Gly Leu Leu Cys Ala Leu
  1   5   10   15

Leu Pro Gln His His Gly Ala Pro Gly Pro Asp Gly Ser Ala Pro
                 20   25   30

Asp Pro Ala His Tyr Ser Phe Ser Leu Thr Leu Ile Asp Ala Leu
                 35   40   45

Asp Thr Leu Leu Ile Leu Gly Asn Val Ser Glu Phe Gln Arg Val
                 50   55   60

Val Glu Val Leu Gln Asp Ser Val Asp Phe Asp Ile Asp Val Asn
                 65   70   75

Ala Ser Val Phe Glu Thr Asn Ile Arg Val Val Gly Gly Leu Leu
                 80   85   90

Ser Ala His Leu Leu Ser Lys Lys Ala Gly Val Glu Val Glu Ala
                 95   100   105

Gly Trp Pro Cys Ser Gly Pro Leu Leu Arg Met Ala Glu Glu Ala
                 110   115   120

Ala Arg Lys Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro
                 125   130   135

Tyr Gly Thr Val Asn Leu Leu His Gly Val Asn Pro Gly Glu Thr
                 140   145   150

Pro Val Thr Cys Thr Ala Gly Ile Gly Thr Phe Ile Val Glu Phe
                 155   160   165

Ala Thr Leu Ser Ser Leu Thr Gly Asp Pro Val Phe Glu Asp Val
                 170   175   180

Ala Arg Val Ala Leu Met Arg Leu Trp Glu Ser Arg Ser Asp Ile
                 185   190   195

Gly Leu Val Gly Asn His Ile Asp Val Leu Thr Gly Lys Trp Val

174

Ala Gln Asp Ala Gly Ile Gly Ala Gly Val Asp Ser Tyr Phe Glu
                215   220   225

Tyr Leu Val Lys Gly Ala Ile Leu Leu Gln Asp Lys Lys Leu Met
                230   235   240

Ala Met Phe Leu Glu Tyr Asn Lys Ala Ile Arg Asn Tyr Thr Arg
                245   250   255

Phe Asp Asp Trp Tyr Leu Trp Val Gln Met Tyr Lys Gly Thr Val
                260   265   270

Ser Met Pro Val Phe Gln Ser Leu Glu Ala Tyr Trp Pro Gly Leu
                275   280   285

Gln Ser Leu Ile Gly Asp Ile Asp Asn Ala Met Arg Thr Phe Leu
                290   295   300

Asn Tyr Tyr Thr Val Trp Lys Gln Phe Gly Gly Leu Pro Glu Phe
                305   310   315

Tyr Asn Ile Pro Gln Gly Tyr Thr Val Glu Lys Arg Glu Gly Tyr
                320   325   330

Pro Leu Arg Pro Glu Leu Ile Glu Ser Ala Met Tyr Leu Tyr Arg
                335   340   345

Ala Thr Gly Asp Pro Thr Leu Leu Glu Leu Gly Arg Asp Ala Val
                350   355   360

Glu Ser Ile Glu Lys Ile Ser Lys Val Glu Cys Gly Phe Ala Thr
                365   370   375

Ile Lys Asp Leu Arg Asp His Lys Leu Asp Asn Arg Met Glu Ser
                380   385   390

Phe Phe Leu Ala Glu Thr Val Lys Tyr Leu Tyr Leu Leu Phe Asp
                395   400   405

Pro Thr Asn Phe Ile His Asn Asn Gly Ser Thr Phe Asp Ala Val
                410   415   420

Ile Thr Pro Tyr Gly Glu Cys Ile Leu Gly Ala Gly Gly Tyr Ile
                425   430   435

Phe Asn Thr Glu Ala His Pro Ile Asp Leu Ala Ala Leu His Cys
                440   445   450

Cys Gln Arg Leu Lys Glu Glu Gln Trp Glu Val Glu Asp Leu Met
                455   460   465

Arg Glu Phe Tyr Ser Leu Lys Arg Ser Arg Ser Lys Phe Gln Lys
                470   475   480

Asn Thr Val Ser Ser Gly Pro Trp Glu Pro Pro Ala Arg Pro Gly
                485   490   495

175

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Thr Leu Phe Ser Pro Glu Asn His Asp Gln Ala Arg Glu Arg Lys
            500                 505                 510

Pro Ala Lys Gln Lys Val Pro Leu Leu Ser Cys Pro Ser Gln Pro
            515                 520                 525

Phe Thr Ser Lys Leu Ala Leu Leu Gly Gln Val Phe Leu Asp Ser
            530                 535                 540

Ser
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<210> 182
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 182

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gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc   150

tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat   200

gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaaa   250

tgcagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcatg   300

tggttttct acgcattgat tccatgtttg ctcacagatg aagtggccat    350

tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc   400

tcttgatgtg agcccagtg atcgcgcctg agaaacagt gtactattct     450

gtcgaatacc aggggagta cgagagcctg tacacgagcc acatctggat    500

ccccagcagc tggtgctcac tcactgaagg tcctgagtgt gatgtcactg   550

atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg   600

ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa   650

ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc   700

acctggttat tgagctggag gacctggggc cccagtttga gttccttgtg   750

gcctactgga ggagggagcc tggtgccgag gaacatgtca aaatggtgag   800

gagtggggggt attccagtgc acctagaaac catggagcca ggggctgcat   850

actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc   900

ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt   950

actggccctg tttgcctttg ttggcttcat gctgatcctt gtggtcgtgc  1000
```

cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050

gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100

aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150

ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200

caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250

aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300

gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggttt 1350

gtctaacaga acactgactg aggcttaggg gatgtgacct ctagactggg 1400

ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcatccctt 1450

cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500

aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550

tacacccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600

tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650

gatcaaggac tctacacact gggtggcttg gagagcccac tttcccagaa 1700

taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750

caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800

gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850

acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900

agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950

gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000

aattcagcaa ataaaaaggg ccaccctggc caaaagcggt aaaaaaaaaa 2050

aaaaaa 2056

<210> 183
<211> 311
<212> PRT
<213> Homo sapiens

<220>
<221> Signal peptide
<222> 1-29
<223> Signal peptide

<220>
<221> N-glycosylation sites
<222> 40-43, 134-137
<223> N-glycosylation sites.

177

<220>
<221> Tissue factor proteins homology
<222> 92-119
<223> Tissue factor proteins homology

<220>
<221> Transmembrane domain
<222> 230-255
<223> Transmembrane domain

<220>
<221> Integrins alpha chain protein homology
<222> 232-262
<223> Integrins alpha chain protein homology

<400> 183
Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu
 1   5   10   15

Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp
                20   25   30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
                35   40   45

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
                50   55   60

Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
                65   70   75

Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
                80   85   90

Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
                95   100   105

Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
                110   115   120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser
                125   130   135

Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe
                140   145   150

His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe
                155   160   165

Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val
                170   175   180

Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met
                185   190   195

Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys
                200   205   210

178

```
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu
              215             220             225

Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
              230             235             240

Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp
              245             250             255

Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val
              260             265             270

Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
              275             280             285

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met
              290             295             300

Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
              305             310
```

<210> 184
<211> 808
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748
<223> unknown base

<400> 184

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cctttctagc ttcctggccg gctctagaac aattcaggct tcgctgcgac 100

tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150

agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250

tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300

gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350

gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400

attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450

tggatcccca gcagctggtg ctcactcact gaaggtcctg agtgtgatgt 500

cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550

cattgggctc acagacctca gcctggagca tcctgaagca tcccttताat 600

agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650
```

```
cttncacctg gttattgagc tggaggacct ggggcccag tttgagttcc 700

ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750

gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800

tgacccac 808
```

<210> 185
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
```
aggcttcgct gcgactagac ctc 23
```

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
```
ccaggtcggg taaggatggt tgag 24
```

<210> 187
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
```
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50
```

<210> 188
<211> 1227
<212> DNA
<213> Homo sapiens

<400> 188
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cggacgcgtg ggccgccacc tccggaacaa gccatggtgg cggcgacggt 50

ggcagcggcg tggctgctcc tgtgggctgc ggcctgcgcg cagcaggagc 100

aggacttcta cgacttcaag gcggtcaaca tccggggcaa actggtgtcg 150

ctggagaagt accgcggatc ggtgtccctg gtggtgaatg tggccagcga 200

gtgcggcttc acagaccagc actaccgagc cctgcagcag ctgcagcgag 250

acctgggccc ccaccacttt aacgtgctcg ccttcccctg caaccagttt 300
```

180

```
ggccaacagg agcctgacag caacaaggag attgagagct ttgcccgccg 350

cacctacagt gtctcattcc ccatgtttag caagattgca gtcaccggta 400

ctggtgccca tcctgccttc aagtacctgg cccagacttc tgggaaggag 450

cccacctgga acttctggaa gtacctagta gccccagatg gaaaggtggt 500

aggggcttgg gacccaactg tgtcagtgga ggaggtcaga ccccagatca 550

cagcgctcgt gaggaagctc atcctactga agcgagaaga cttataacca 600

ccgcgtctcc tcctccacca cctcatcccg cccacctgtg tggggctgac 650

caatgcaaac tcaaatggtg cttcaaaggg agagacccac tgactctcct 700

tcctttactc ttatgccatt ggtcccatca ttcttgtggg ggaaaaattc 750

tagtattttg attatttgaa tcttacagca acaaatagga actcctggcc 800

aatgagagct cttgaccagt gaatcaccag ccgatacgaa cgtcttgcca 850

acaaaaatgt gtggcaaata gaagtatatc aagcaataat ctcccaccca 900

aggcttctgt aaactgggac caatgattac ctcatagggc tgttgtgagg 950

attaggatga aatacctgtg aaagtgccta ggcagtgcca gccaaatagg 1000

aggcattcaa tgaacatttt ttgcatataa accaaaaaat aacttgttat 1050

caataaaaac ttgcatccaa catgaatttc cagccgatga taatccaggc 1100

caaaggttta gttgttgtta tttcctctgt attattttct tcattacaaa 1150

agaaatgcaa gttcattgta acaatccaaa caatacctca cgatataaaa 1200

taaaaatgaa agtatcctcc tcaaaaa 1227
```

<210> 189
<211> 187
<212> PRT
<213> Homo sapiens

<400> 189

```
Met Val Ala Ala Thr Val Ala Ala Ala Trp Leu Leu Leu Trp Ala
 1               5                  10                  15

Ala Ala Cys Ala Gln Gln Glu Gln Asp Phe Tyr Asp Phe Lys Ala
                20                  25                  30

Val Asn Ile Arg Gly Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly
                35                  40                  45

Ser Val Ser Leu Val Val Asn Val Ala Ser Glu Cys Gly Phe Thr
                50                  55                  60

Asp Gln His Tyr Arg Ala Leu Gln Gln Leu Gln Arg Asp Leu Gly
                65                  70                  75
```

181

```
Pro His His Phe Asn Val Leu Ala Phe Pro Cys Asn Gln Phe Gly
                80                  85                  90

Gln Gln Glu Pro Asp Ser Asn Lys Glu Ile Glu Ser Phe Ala Arg
                95                  100                 105

Arg Thr Tyr Ser Val Ser Phe Pro Met Phe Ser Lys Ile Ala Val
                110                 115                 120

Thr Gly Thr Gly Ala His Pro Ala Phe Lys Tyr Leu Ala Gln Thr
                125                 130                 135

Ser Gly Lys Glu Pro Thr Trp Asn Phe Trp Lys Tyr Leu Val Ala
                140                 145                 150

Pro Asp Gly Lys Val Val Gly Ala Trp Asp Pro Thr Val Ser Val
                155                 160                 165

Glu Glu Val Arg Pro Gln Ile Thr Ala Leu Val Arg Lys Leu Ile
                170                 175                 180

Leu Leu Lys Arg Glu Asp Leu
                185

<210> 190
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 190
 gcaggacttc tacgacttca aggc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 191
 agtctgggcc aggtacttga aggc 24

<210> 192
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
 caacatccgg ggcaaactgg tgtcgctgga gaagtaccgc ggatcggtgt 50

<210> 193
```

182

<211> 2187
<212> DNA
<213> Homo sapiens

<400> 193
cggacgcgtg ggcgggccgg gacgcagggc aaagcgagcc atggctgtct 50

acgtcgggat gctgcgcctg gggaggctgt gcgccgggag ctcggggggtg 100

ctggggggccc gggccgccct ctctcggagt tggcaggaag ccaggttgca 150

gggtgtccgc ttcctcagtt ccagagaggt ggatcgcatg gtctccacgc 200

ccatcggagg cctcagctac gttcaggggt gcaccaaaaa gcatcttaac 250

agcaagactg tgggccagtg cctggagacc acagcacaga gggtcccaga 300

acgagaggcc ttggtcgtcc tccatgaaga cgtcaggttg acctttgccc 350

aactcaagga ggaggtggac aaagctgctt ctggcctcct gagcattggc 400

ctctgcaaag gtgaccggct gggcatgtgg ggacctaact cctatgcatg 450

ggtgctcatg cagttggcca ccgcccaggc gggcatcatt ctggtgtctg 500

tgaacccagc ctaccaggct atggaactgg agtatgtcct caagaaggtg 550

ggctgcaagg cccttgtgtt ccccaagcaa ttcaagaccc agcaatacta 600

caacgtcctg aagcagatct gtccagaagt ggagaatgcc cagccagggg 650

ccttgaagag tcagaggctc ccagatctga ccacagtcat ctcggtggat 700

gccccttttgc cggggaccct gctcctggat gaagtggtgg cggctggcag 750

cacacggcag catctggacc agctccaata caaccagcag ttcctgtcct 800

gccatgaccc catcaacatc cagttcacct cggggacaac aggcagcccc 850

aagggggcca ccctctccca ctacaacatt gtcaacaact ccaacatttt 900

aggagagcgc ctgaaactgc atgagaagac accagagcag ttgcggatga 950

tcctgcccaa ccccctgtac cattgcctgg gttccgtggc aggcacaatg 1000

atgtgtctga tgtacggtgc caccctcatc ctggcctctc ccatcttcaa 1050

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acctccagag ttgatccgag ccatcatcaa caagataaat atgaaggacc 1250

tggtggttgc ttatggaacc acagagaaca gtcccgtgac attcgcgcac 1300

ttccctgagg acactgtgga gcagaaggca gaaagcgtgg gcagaattat 1350

183

```
gcctcacacg gaggcccgga tcatgaacat ggaggcaggg acgctggcaa 1400

agctgaacac gcccggggag ctgtgcatcc gagggtactg cgtcatgctg 1450

ggctactggg gtgagcctca gaagacagag gaagcagtgg atcaggacaa 1500

gtggtattgg acaggagatg tcgccacaat gaatgagcag ggcttctgca 1550

agatcgtggg ccgctctaag gatatgatca tccggggtgg tgagaacatc 1600

taccccgcag agctcgagga cttctttcac acacacccga aggtgcagga 1650

agtgcaggtg gtgggagtga aggacgatcg gatgggggaa gagatttgtg 1700

cctgcattcg gctgaaggac ggggaggaga ccacggtgga ggagataaaa 1750

gctttctgca aagggaagat ctctcacttc aagattccga agtacatcgt 1800

gtttgtcaca aactaccccc tcaccatttc aggaaagatc cagaaattca 1850

aacttcgaga gcagatggaa cgacatctaa atctgtgaat aaagcagcag 1900

gcctgtcctg gccggttggc ttgactctct cctgtcagaa tgcaacctgg 1950

ctttatgcac ctagatgtcc ccagcaccca gttctgagcc aggcacatca 2000

aatgtcaagg aattgactga acgaactaag agctcctgga tgggtccggg 2050

aactcgcctg ggcacaaggt gccaaaaggc aggcagcctg cccaggccct 2100

ccctcctgtc catcccccac attcccctgt ctgtccttgt gatttggcat 2150

aaagagcttc tgttttcttt gaaaaaaaaa aaaaaaa 2187
```

<210> 194
<211> 615
<212> PRT
<213> Homo sapiens

<400> 194
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Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala
 1               5                  10                  15

Gly Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser
                20                  25                  30

Trp Gln Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg
                35                  40                  45

Glu Val Asp Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr
                50                  55                  60

Val Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly
                65                  70                  75

Gln Cys Leu Glu Thr Thr Ala Gln Arg Val Pro Glu Arg Glu Ala
                80                  85                  90
```

Leu Val Val Leu His Glu Asp Val Arg Leu Thr Phe Ala Gln Leu
                95   100   105

Lys Glu Glu Val Asp Lys Ala Ala Ser Gly Leu Leu Ser Ile Gly
                110   115   120

Leu Cys Lys Gly Asp Arg Leu Gly Met Trp Gly Pro Asn Ser Tyr
                125   130   135

Ala Trp Val Leu Met Gln Leu Ala Thr Ala Gln Ala Gly Ile Ile
                140   145   150

Leu Val Ser Val Asn Pro Ala Tyr Gln Ala Met Glu Leu Glu Tyr
                155   160   165

Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val Phe Pro Lys Gln
                170   175   180

Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln Ile Cys Pro
                185   190   195

Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln Arg Leu
                200   205   210

Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro Gly
                215   220   225

Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
                230   235   240

His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His
                245   250   255

Asp Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro
                260   265   270

Lys Gly Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn
                275   280   285

Ile Leu Gly Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln
                290   295   300

Leu Arg Met Ile Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser
                305   310   315

Val Ala Gly Thr Met Met Cys Leu Met Tyr Gly Ala Thr Leu Ile
                320   325   330

Leu Ala Ser Pro Ile Phe Asn Gly Lys Lys Ala Leu Glu Ala Ile
                335   340   345

Ser Arg Glu Arg Gly Thr Phe Leu Tyr Gly Thr Pro Thr Met Phe
                350   355   360

Val Asp Ile Leu Asn Gln Pro Asp Phe Ser Ser Tyr Asp Ile Ser
                365   370   375

Thr Met Cys Gly Gly Val Ile Ala Gly Ser Pro Ala Pro Pro Glu

185

```
Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn Met Lys Asp Leu Val
                395                400                405

Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val Thr Phe Ala His
                410                415                420

Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser Val Gly Arg
                425                430                435

Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu Ala Gly
                440                445                450

Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg Gly
                455                460                465

Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu
                470                475                480

Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala
                485                490                495

Thr Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys
                500                505                510

Asp Met Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu
                515                520                525

Glu Asp Phe Phe His Thr His Pro Lys Val Gln Glu Val Gln Val
                530                535                540

Val Gly Val Lys Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys
                545                550                555

Ile Arg Leu Lys Asp Gly Glu Glu Thr Thr Val Glu Glu Ile Lys
                560                565                570

Ala Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr
                575                580                585

Ile Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile
                590                595                600

Gln Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu
                605                610                615
```

```
<210> 195
<211> 642
<212> DNA
<213> Homo sapiens

<400> 195
 caactccaac attttaggag agcgcctgaa actgcatgag aagacaccag 50

 agcagttgcg gatgatcctg cccaaccccc tgtaccattg cctgggttcc 100

 gtggcaggca caatgatgtg tctgatgtac ggtgccaccc tcatcctggc 150
```

ctctcccatc ttcaatggca agaaggcact ggaggccatc agcagagaga 200

gaggcacctt cctgtatggt accccacga tgttcgtgga cattctgaac 250

cagccagact tctccagtta tgacatctcg accatgtgtg gaggtgtcat 300

tgctgggtcc cctgcacctc cagagttgat ccgagccatc atcaacaaga 350

taaatatgaa ggacctggtg gttgcttatg aaccacaga gaacagtccc 400

gtgacattcg cgcacttccc tgaggacact gtggagcaga aggcagaaag 450

cgtgggcaga attatgcctc acacggaggc gcggatcatg aacatggagg 500

cagggacgct ggcaaagctg aacacgcccg gggagctgtg catccgaggg 550

tactgcgtca tgctgggcta ctggggtgag cctcagaaga cagaggaagc 600

agtggatcag gacaagtggt attggacagg agatgtcgcc ac 642

<210> 196
<211> 1575
<212> DNA
<213> Homo sapiens

<400> 196
gagcaggacg gagccatgga ccccgccagg aaagcaggtg cccaggccat 50

gatctggact gcaggctggc tgctgctgct gctgcttcgc ggaggagcgc 100

aggccctgga gtgctacagc tgcgtgcaga aagcagatga cggatgctcc 150

ccgaacaaga tgaagacagt gaagtgcgcg ccgggcgtgg acgtctgcac 200

cgaggccgtg ggggcggtgg agaccatcca cggacaattc tcgctggcag 250

tgcggggttg cggttcggga ctccccggca agaatgaccg cggcctggat 300

cttcacgggc ttctggcgtt catccagctg cagcaatgcg ctcaggatcg 350

ctgcaacgcc aagctcaacc tcacctcgcg ggcgctcgac ccggcaggta 400

atgagagtgc atacccgccc aacggcgtgg agtgctacag ctgtgtgggc 450

ctgagccggg aggcgtgcca gggtacatcg ccgccggtcg tgagctgcta 500

caacgccagc gatcatgtct acaagggctg cttcgacggc aacgtcacct 550

tgacggcagc taatgtgact gtgtccttgc ctgtccgggg ctgtgtccag 600

gatgaattct gcactcggga tggagtaaca ggcccagggt tcacgctcag 650

tggctcctgt tgccaggggt cccgctgtaa ctctgacctc cgcaacaaga 700

cctacttctc ccctcgaatc ccacccttg tccggctgcc ccctccagag 750

cccacgactg tggcctcaac cacatctgtc accacttcta cctcggcccc 800

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agtgagaccc acatccacca ccaaacccat gccagcgcca accagtcaga 850

ctccgagaca gggagtagaa cacgaggcct cccgggatga ggagcccagg 900

ttgactggag gcgccgctgg ccaccaggac cgcagcaatt cagggcagta 950

tcctgcaaaa gggggggcccc agcagcccca taataaaggc tgtgtggctc 1000

ccacagctgg attggcagcc cttctgttgg ccgtggctgc tggtgtccta 1050

ctgtgagctt ctccacctgg aaatttccct ctcacctact tctctggccc 1100

tgggtacccc tcttctcatc acttcctgtt cccaccactg gactgggctg 1150

gcccagcccc tgttttttcca acattcccca gtatccccag cttctgctgc 1200

gctggtttgc ggctttggga aataaaatac cgttgtatat attctgccag 1250

gggtgttcta gcttttttgag gacagctcct gtatccttct catccttgtc 1300

tctccgcttg tcctcttgtg atgttaggac agagtgagag aagtcagctg 1350

tcacggggaa ggtgagagag aggatgctaa gcttcctact cactttctcc 1400

tagccagcct ggactttgga gcgtggggtg ggtgggacaa tggctccccca 1450

ctctaagcac tgcctcccct actccccgca tctttgggga atcggttccc 1500

catatgtctt ccttactaga ctgtgagctc ctcgaggggg ggcccggtac 1550

ccaattcgcc ctatagtgag tcgta 1575
```

<210> 197
<211> 346
<212> PRT
<213> Homo sapiens

<400> 197

```
Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr
 1               5                   10                  15

Ala Gly Trp Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala
                20                  25                  30

Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser
                35                  40                  45

Pro Asn Lys Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val
                50                  55                  60

Cys Thr Glu Ala Val Gly Ala Val Glu Thr Ile His Gly Gln Phe
                65                  70                  75

Ser Leu Ala Val Arg Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn
                80                  85                  90

Asp Arg Gly Leu Asp Leu His Gly Leu Leu Ala Phe Ile Gln Leu
                95                  100                 105
```

188

```
Gln Gln Cys Ala Gln Asp Arg Cys Asn Ala Lys Leu Asn Leu Thr
            110                 115                     120

Ser Arg Ala Leu Asp Pro Ala Gly Asn Glu Ser Ala Tyr Pro Pro
            125                 130                     135

Asn Gly Val Glu Cys Tyr Ser Cys Val Gly Leu Ser Arg Glu Ala
            140                 145                     150

Cys Gln Gly Thr Ser Pro Pro Val Val Ser Cys Tyr Asn Ala Ser
            155                 160                     165

Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn Val Thr Leu Thr
            170                 175                     180

Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly Cys Val Gln
            185                 190                     195

Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly Phe Thr
            200                 205                     210

Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp Leu
            215                 220                     225

Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
            230                 235                     240

Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val
            245                 250                     255

Thr Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys
            260                 265                     270

Pro Met Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu
            275                 280                     285

His Glu Ala Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala
            290                 295                     300

Ala Gly His Gln Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys
            305                 310                     315

Gly Gly Pro Gln Gln Pro His Asn Lys Gly Cys Val Ala Pro Thr
            320                 325                     330

Ala Gly Leu Ala Ala Leu Leu Leu Ala Val Ala Ala Gly Val Leu
            335                 340                     345

Leu
```

<210> 198
<211> 1657
<212> DNA
<213> Homo sapiens

<400> 198
cgggactcgg cgggtcctcc tgggagtctc ggaggggacc ggctgtgcag 50

189

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acgccatgga gttggtgctg gtcttcctct gcagcctgct ggcccccatg 100

gtcctggcca gtgcagctga aaaggagaag gaaatggacc cttttcatta 150

tgattaccag accctgagga ttgggggact ggtgttcgct gtggtcctct 200

tctcggttgg gatcctcctt atcctaagtc gcaggtgcaa gtgcagtttc 250

aatcagaagc cccgggcccc aggagatgag gaagcccagg tggagaacct 300

catcaccgcc aatgcaacag agccccagaa gcagagaact gaagtgcagc 350

catcaggtgg aagcctctgg aacctgaggc ggctgcttga acctttggat 400

gcaaatgtcg atgcttaaga aaaccggcca cttcagcaac agccctttcc 450

ccaggagaag ccaagaactt gtgtgtcccc caccctatcc cctctaacac 500

cattcctcca cctgatgatg caactaacac ttgcctcccc actgcagcct 550

gcggtcctgc ccacctcccg tgatgtgtgt gtgtgtgtgt gtgtgtgact 600

gtgtgtgttt gctaactgtg gtctttgtgg ctacttgttt gtggatggta 650

ttgtgtttgt tagtgaactg tggactcgct ttcccaggca ggggctgagc 700

cacatggcca tctgctcctc cctgcccccg tggccctcca tcaccttctg 750

ctcctaggag gctgcttgtt gcccgagacc agccccctcc cctgatttag 800

ggatgcgtag ggtaagagca cgggcagtgg tcttcagtcg tcttgggacc 850

tgggaaggtt tgcagcactt tgtcatcatt cttcatggac tcctttcact 900

cctttaacaa aaaccttgct tccttatccc acctgatccc agtctgaagg 950

tctcttagca actggagata caaagcaagg agctggtgag cccagcgttg 1000

acgtcaggca ggctatgccc ttccgtggtt aatttcttcc cagggcttc 1050

cacgaggagt ccccatctgc cccgcccctt cacagagcgc ccggggattc 1100

caggcccagg gcttctactc tgcccctggg gaatgtgtcc cctgcatatc 1150

ttctcagcaa taactccatg ggctctggga ccctacccct tccaaccttc 1200

cctgcttctg agacttcaat ctacagccca gctcatccag atgcagacta 1250

cagtccctgc aattgggtct ctggcaggca atagttgaag gactcctgtt 1300

ccgttggggc cagcacaccg ggatggatgg agggagagca gaggcctttg 1350

cttctctgcc tacgtcccct tagatgggca gcagaggcaa ctcccgcatc 1400

ctttgctctg cctgtcggtg gtcagagcgg tgagcgaggt gggttggaga 1450

ctcagcaggc tccgtgcagc ccttgggaac agtgagaggt tgaaggtcat 1500
```

190

```
aacgagagtg ggaactcaac ccagatcccg cccctcctgt cctctgtgtt 1550

cccgcggaaa ccaaccaaac cgtgcgctgt gacccattgc tgttctctgt 1600

atcgtgatct atcctcaaca acaacagaaa aaaggaataa aatatccttt 1650

gtttcct 1657
```

<210> 199
<211> 120
<212> PRT
<213> Homo sapiens

<400> 199
```
Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met
  1               5                  10                  15

Val Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe
                 20                  25                  30

His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala
                 35                  40                  45

Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg
                 50                  55                  60

Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu
                 65                  70                  75

Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro
                 80                  85                  90

Gln Lys Gln Arg Thr Glu Val Gln Pro Ser Gly Gly Ser Leu Trp
                 95                 100                 105

Asn Leu Arg Arg Leu Leu Glu Pro Leu Asp Ala Asn Val Asp Ala
                110                 115                 120
```

<210> 200
<211> 415
<212> DNA
<213> Homo sapiens

<400> 200
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aaacttgacg ccatgaagat cccggtcctt cctgccgtgg tgctcctctc 50

cctcctggtg ctccactctg cccagggagc caccctgggt ggtcctgagg 100

aagaaagcac cattgagaat tatgcgtcac gacccgaggc ctttaacacc 150

ccgttcctga acatcgacaa attgcgatct gcgtttaagg ctgatgagtt 200

cctgaactgg cacgccctct ttgagtctat caaaaggaaa cttcctttcc 250

tcaactggga tgcctttcct aagctgaaag gactgaggag cgcaactcct 300

gatgcccagt gaccatgacc tccactggaa gagggggcta gcgtgagcgc 350
```

191

tgattctcaa cctaccataa ctctttcctg cctcaggaac tccaataaaa 400

cattttccat ccaaa 415

<210> 201
<211> 99
<212> PRT
<213> Homo sapiens

<400> 201
 Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu
 1   5   10   15

 Val Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu
                 20   25   30

 Glu Ser Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn
                 35   40   45

 Thr Pro Phe Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala
                 50   55   60

 Asp Glu Phe Leu Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg
                 65   70   75

 Lys Leu Pro Phe Leu Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly
                 80   85   90

 Leu Arg Ser Ala Thr Pro Asp Ala Gln
                 95

<210> 202
<211> 678
<212> DNA
<213> Homo sapiens

<400> 202
 cagttctgaa atcaatggag ttaatttagg gaatacaaac cagccatggg 50

 ggtggagatt gcctttgcct cagtgattct cacctgcctc tcccttctgg 100

 cagcaggagt ctcccaggtt gttcttctcc agccagttcc aactcaggag 150

 acaggtccca aggccatggg agatctctcc tgtggctttg ccggccactc 200

 atgagagtgt ttttgtgtaa agtatttttt agaatactgt tgacttcttc 250

 atgatttaat aaccatcctt tgcgaagttt tatgaggctt tagggggaatg 300

 tcaaccctca aattttgtt atactagatg gcttccattt acccaccact 350

 attttaaggt cctttatttt ttaggttcaa ggttcatttg acttgagaaa 400

 gtgcccttct gcagcttcat tgattttgtt tatcttcact attaattgta 450

 acgattaaaa aagaataaga gcacgcagac tctaggaga atattttatc 500

 cctgggtgcc cctgacacat ttatgtagtg atcccacaaa tgtgattgtt 550

aatttaaatg ttattctaat attagtacat tcagttgtga tgtaatatga 600

ataaccagaa tctatttctt aaaagttttg agtatatttt tcaactagat 650

atttgtatag aaagactgaa tagtgatg 678

<210> 203
<211> 52
<212> PRT
<213> Homo sapiens

<400> 203
```
Met Gly Val Glu Ile Ala Phe Ala Ser Val Ile Leu Thr Cys Leu
 1               5                  10                  15

Ser Leu Leu Ala Ala Gly Val Ser Gln Val Val Leu Leu Gln Pro
                20                  25                  30

Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser
                35                  40                  45

Cys Gly Phe Ala Gly His Ser
                50
```

<210> 204
<211> 1917
<212> DNA
<213> Homo sapiens

<400> 204
ggggaatctg cagtaggtct gccggcgatg gagtggtggg ctagctcgcc 50

gcttcggctc tggctgctgt tgttcctcct gccctcagcg cagggccgcc 100

agaaggagtc aggttcaaaa tggaaagtat ttattgacca aattaacagg 150

tctttggaga attacgaacc atgttcaagt caaaactgca gctgctacca 200

tggtgtcata gaagaggatc taactccttt ccgaggaggc atctccagga 250

agatgatggc agaggtagtc agacggaagc tagggaccca ctatcagatc 300

actaagaaca gactgtaccg ggaaaatgac tgcatgttcc cctcaaggtg 350

tagtggtgtt gagcacttta ttttggaagt gatcgggcgt ctccctgaca 400

tggagatggt gatcaatgta cgagattatc ctcaggttcc taaatggatg 450

gagcctgcca tcccagtctt ctccttcagt aagacatcag agtaccatga 500

tatcatgtat cctgcttgga cattttggga aggggggacct gctgtttggc 550

caatttatcc tacaggtctt ggacggtggg acctcttcag agaagatctg 600

gtaaggtcag cagcacagtg gccatggaaa aagaaaaact ctacagcata 650

tttccgagga tcaaggacaa gtccagaacg agatcctctc attcttctgt 700
```

```
ctcggaaaaa cccaaaactt gttgatgcag aatacaccaa aaaccaggcc 750

tggaaatcta tgaaagatac cttaggaaag ccagctgcta aggatgtcca 800

tcttgtggat cactgcaaat acaagtatct gtttaatttt cgaggcgtag 850

ctgcaagttt ccggtttaaa cacctcttcc tgtgtggctc acttgttttc 900

catgttggtg atgagtggct agaattcttc tatccacagc tgaagccatg 950

ggttcactat atcccagtca aaacagatct ctccaatgtc caagagctgt 1000

tacaatttgt aaaagcaaat gatgatgtag ctcaagagat tgctgaaagg 1050

ggaagccagt ttattaggaa ccatttgcag atggatgaca tcacctgtta 1100

ctgggagaac ctcttgagtg aatactctaa attcctgtct tataatgtaa 1150

cgagaaggaa aggttatgat caaattattc ccaaaatgtt gaaaactgaa 1200

ctatagtagt catcatagga ccatagtcct ctttgtggca acagatctca 1250

gatatcctac ggtgagaagc ttaccataag cttggctcct ataccttgaa 1300

tatctgctat caagccaaat acctggtttt ccttatcatg ctgcacccag 1350

agcaactctt gagaaagatt taaaatgtgt ctaatacact gatatgaagc 1400

agttcaactt tttggatgaa taaggaccag aaatcgtgag atgtggattt 1450

tgaacccaac tctacctttc attttcttaa gaccaatcac agcttgtgcc 1500

tcagatcatc cacctgtgtg agtccatcac tgtgaaattg actgtgtcca 1550

tgtgatgatg ccctttgtcc cattatttgg agcagaaaat tcgtcatttg 1600

gaagtagtac aactcattgc tggaattgtg aaattattca aggcgtgatc 1650

tctgtcactt tattttaatg taggaaaccc tatggggttt atgaaaaata 1700

cttggggatc attctctgaa tggtctaagg aagcggtagc catgccatgc 1750

aatgatgtag gagttctctt ttgtaaaacc ataaactctg ttactcagga 1800

ggtttctata atgccacata gaaagaggcc aattgcatga gtaattattg 1850

caattggatt tcaggttccc tttttgtgcc ttcatgccct acttcttaat 1900

gcctctctaa agccaaa 1917
```

<210> 205
<211> 392
<212> PRT
<213> Homo sapiens

<400> 205

```
Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu Trp Leu Leu Leu
1               5                   10                  15
```

194

Phe Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser
                    20   25   30

Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn
                    35   40   45

Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val
                    50   55   60

Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys
                    65   70   75

Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln
                    80   85   90

Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro
                    95   100   105

Ser Arg Cys Ser Gly Val Glu His Phe Ile Leu Glu Val Ile Gly
                    110   115   120

Arg Leu Pro Asp Met Glu Met Val Ile Asn Val Arg Asp Tyr Pro
                    125   130   135

Gln Val Pro Lys Trp Met Glu Pro Ala Ile Pro Val Phe Ser Phe
                    140   145   150

Ser Lys Thr Ser Glu Tyr His Asp Ile Met Tyr Pro Ala Trp Thr
                    155   160   165

Phe Trp Glu Gly Gly Pro Ala Val Trp Pro Ile Tyr Pro Thr Gly
                    170   175   180

Leu Gly Arg Trp Asp Leu Phe Arg Glu Asp Leu Val Arg Ser Ala
                    185   190   195

Ala Gln Trp Pro Trp Lys Lys Lys Asn Ser Thr Ala Tyr Phe Arg
                    200   205   210

Gly Ser Arg Thr Ser Pro Glu Arg Asp Pro Leu Ile Leu Leu Ser
                    215   220   225

Arg Lys Asn Pro Lys Leu Val Asp Ala Glu Tyr Thr Lys Asn Gln
                    230   235   240

Ala Trp Lys Ser Met Lys Asp Thr Leu Gly Lys Pro Ala Ala Lys
                    245   250   255

Asp Val His Leu Val Asp His Cys Lys Tyr Lys Tyr Leu Phe Asn
                    260   265   270

Phe Arg Gly Val Ala Ala Ser Phe Arg Phe Lys His Leu Phe Leu
                    275   280   285

Cys Gly Ser Leu Val Phe His Val Gly Asp Glu Trp Leu Glu Phe
                    290   295   300

Phe Tyr Pro Gln Leu Lys Pro Trp Val His Tyr Ile Pro Val Lys

195

```
Thr Asp Leu Ser Asn Val Gln Glu Leu Leu Gln Phe Val Lys Ala
                320                 325                 330

Asn Asp Asp Val Ala Gln Glu Ile Ala Glu Arg Gly Ser Gln Phe
                335                 340                 345

Ile Arg Asn His Leu Gln Met Asp Asp Ile Thr Cys Tyr Trp Glu
                350                 355                 360

Asn Leu Leu Ser Glu Tyr Ser Lys Phe Leu Ser Tyr Asn Val Thr
                365                 370                 375

Arg Arg Lys Gly Tyr Asp Gln Ile Ile Pro Lys Met Leu Lys Thr
                380                 385                 390

Glu Leu
```

```
<210> 206
<211> 1425
<212> DNA
<213> Homo sapiens

<400> 206
 cacccctcca tttctcgcca tggcccctgc actgctcctg atccctgctg 50

 ccctcgcctc tttcatcctg gcctttggca ccggagtgga gttcgtgcgc 100

 tttacctccc ttcggccact tcttggaggg atcccggagt ctggtggtcc 150

 ggatgcccgc cagggatggc tggctgccct gcaggaccgc agcatccttg 200

 cccccctggc atgggatctg gggctcctgc ttctatttgt tgggcagcac 250

 agcctcatgg cagctgaaag agtgaaggca tggacatccc ggtactttgg 300

 ggtccttcag aggtcactgt atgtggcctg cactgccctg gccttgcagc 350

 tggtgatgcg gtactgggag cccatcccca aaggccctgt gttgtgggag 400

 gctcgggctg agccatgggc cacctgggtg ccgctcctct gctttgtgct 450

 ccatgtcatc tcctggctcc tcatctttag catccttctc gtctttgact 500

 atgctgagct catgggcctc aaacaggtat actaccatgt gctggggctg 550

 ggcgagcctc tggccctgaa gtctccccgg gctctcagac tcttctccca 600

 cctgcgccac ccagtgtgtg tggagctgct gacagtgctg tgggtggtgc 650

 ctaccctggg cacggaccgt ctcctccttg ctttcctcct taccctctac 700

 ctgggcctgg ctcacgggct tgatcagcaa gacctccgct acctccgggc 750

 ccagctacaa agaaaactcc acctgctctc tcggccccag gatggggagg 800
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cagagtgagg agctcactct ggttacaagc cctgttcttc ctctcccact 850

gaattctaaa tccttaacat ccaggccctg gctgcttcat gccagaggcc 900

caaatccatg gactgaagga gatgcccctt ctactacttg agactttatt 950

ctctgggtcc agctccatac cctaaattct gagtttcagc cactgaactc 1000

caaggtccac ttctcaccag caaggaagag tggggtatgg aagtcatctg 1050

tcccttcact gtttagagca tgacactctc cccctcaaca gcctcctgag 1100

aaggaaagga tctgccctga ccactcccct ggcactgtta cttgcctctg 1150

cgcctcaggg gtccccttct gcaccgctgg cttccactcc aagaaggtgg 1200

accagggtct gcaagttcaa cggtcatagc tgtccctcca ggccccaacc 1250

ttgcctcacc actcccggcc ctagtctctg cacctcctta ggccctgcct 1300

ctgggctcag accccaacct agtcaagggg attctcctgc tcttaactcg 1350

atgacttggg gctccctgct ctcccgagga agatgctctg caggaaaata 1400

aaagtcagcc ttttctaaa aaaaa 1425

<210> 207
<211> 262
<212> PRT
<213> Homo sapiens

<400> 207
Met Ala Pro Ala Leu Leu Leu Ile Pro Ala Ala Leu Ala Ser Phe
1   5   10   15

Ile Leu Ala Phe Gly Thr Gly Val Glu Phe Val Arg Phe Thr Ser
                20   25   30

Leu Arg Pro Leu Leu Gly Gly Ile Pro Glu Ser Gly Gly Pro Asp
                35   40   45

Ala Arg Gln Gly Trp Leu Ala Ala Leu Gln Asp Arg Ser Ile Leu
                50   55   60

Ala Pro Leu Ala Trp Asp Leu Gly Leu Leu Leu Leu Phe Val Gly
                65   70   75

Gln His Ser Leu Met Ala Ala Glu Arg Val Lys Ala Trp Thr Ser
                80   85   90

Arg Tyr Phe Gly Val Leu Gln Arg Ser Leu Tyr Val Ala Cys Thr
                95   100   105

Ala Leu Ala Leu Gln Leu Val Met Arg Tyr Trp Glu Pro Ile Pro
                110   115   120

Lys Gly Pro Val Leu Trp Glu Ala Arg Ala Glu Pro Trp Ala Thr
                125   130   135

197

Trp Val Pro Leu Leu Cys Phe Val Leu His Val Ile Ser Trp Leu
            140   145   150

Leu Ile Phe Ser Ile Leu Leu Val Phe Asp Tyr Ala Glu Leu Met
            155   160   165

Gly Leu Lys Gln Val Tyr Tyr His Val Leu Gly Leu Gly Glu Pro
            170   175   180

Leu Ala Leu Lys Ser Pro Arg Ala Leu Arg Leu Phe Ser His Leu
            185   190   195

Arg His Pro Val Cys Val Glu Leu Leu Thr Val Leu Trp Val Val
            200   205   210

Pro Thr Leu Gly Thr Asp Arg Leu Leu Leu Ala Phe Leu Leu Thr
            215   220   225

Leu Tyr Leu Gly Leu Ala His Gly Leu Asp Gln Gln Asp Leu Arg
            230   235   240

Tyr Leu Arg Ala Gln Leu Gln Arg Lys Leu His Leu Leu Ser Arg
            245   250   255

Pro Gln Asp Gly Glu Ala Glu
            260

<210> 208
<211> 2095
<212> DNA
<213> Homo sapiens

<400> 208
ccgagcacag gagattgcct gcgtttagga ggtggctgcg ttgtgggaaa 50

agctatcaag gaagaaattg ccaaaccatg tcttttttc tgttttcaga 100

gtagttcaca acagatctga gtgttttaat taagcatgga atacagaaaa 150

caacaaaaaa cttaagcttt aatttcatct ggaattccac agttttctta 200

gctccctgga cccggttgac ctgttggctc ttcccgctgg ctgctctatc 250

acgtggtgct ctccgactac tcaccccgag tgtaaagaac cttcggctcg 300

cgtgcttctg agctgctgtg gatggcctcg gctctctgga ctgtccttcc 350

gagtaggatg tcactgagat ccctcaaatg gagcctcctg ctgctgtcac 400

tcctgagttt ctttgtgatg tggtacctca gccttcccca ctacaatgtg 450

atagaacgcg tgaactggat gtacttctat gagtatgagc cgatttacag 500

acaagacttt cacttcacac ttcgagagca ttcaaactgc tctcatcaaa 550

atccatttct ggtcattctg gtgacctccc acccttcaga tgtgaaagcc 600

aggcaggcca ttagagttac ttggggtgaa aaaaagtctt ggtggggata 650

198

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tgaggttctt acatttttct tattaggcca agaggctgaa aaggaagaca 700

aaatgttggc attgtcctta gaggatgaac accttcttta tggtgacata 750

atccgacaag atttttaga cacatataat aacctgacct tgaaaaccat 800

tatggcattc aggtgggtaa ctgagttttg ccccaatgcc aagtacgtaa 850

tgaagacaga cactgatgtt ttcatcaata ctggcaattt agtgaagtat 900

cttttaaacc taaaccactc agagaagttt ttcacaggtt atcctctaat 950

tgataattat tcctatagag gattttacca aaaaacccat atttcttacc 1000

aggagtatcc tttcaaggtg ttccctccat actgcagtgg gttgggttat 1050

ataatgtcca gagatttggt gccaaggatc tatgaaatga tgggtcacgt 1100

aaaacccatc aagtttgaag atgtttatgt cgggatctgt ttgaatttat 1150

taaaagtgaa cattcatatt ccagaagaca caaatctttt ctttctatat 1200

agaatccatt tggatgtctg tcaactgaga cgtgtgattg cagcccatgg 1250

cttttcttcc aaggagatca tcactttttg gcaggtcatg ctaaggaaca 1300

ccacatgcca ttattaactt cacattctac aaaaagccta gaaggacagg 1350

ataccttgtg gaaagtgtta aataaagtag gtactgtgga aaattcatgg 1400

ggaggtcagt gtgctggctt acactgaact gaaactcatg aaaaacccag 1450

actggagact ggagggttac acttgtgatt tattagtcag gcccttcaaa 1500

gatgatatgt ggaggaatta aatataaagg aattggaggt ttttgctaaa 1550

gaaattaata ggaccaaaca atttggacat gtcattctgt agactagaat 1600

ttcttaaaag ggtgttactg agttataagc tcactaggct gtaaaaacaa 1650

aacaatgtag agttttattt attgaacaat gtagtcactt gaaggttttg 1700

tgtatatctt atgtggatta ccaatttaaa aatatatgta gttctgtgtc 1750

aaaaaacttc ttcactgaag ttatactgaa caaaatttta cctgtttttg 1800

gtcatttata aagtacttca agatgttgca gtatttcaca gttattatta 1850

tttaaaatta cttcaacttt gtgtttttaa atgttttgac gatttcaata 1900

caagataaaa aggatagtga atcattcttt acatgcaaac attttccagt 1950

tacttaactg atcagtttat tattgataca tcactccatt aatgtaaagt 2000

cataggtcat tattgcatat cagtaatctc ttggactttg ttaaatattt 2050

tactgtggta atatagagaa gaattaaagc aagaaaatct gaaaa 2095
```

199

<210> 209
<211> 331
<212> PRT
<213> Homo sapiens

<400> 209
Met Ala Ser Ala Leu Trp Thr Val Leu Pro Ser Arg Met Ser Leu
 1   5   10   15

Arg Ser Leu Lys Trp Ser Leu Leu Leu Ser Leu Leu Ser Phe
                20   25   30

Phe Val Met Trp Tyr Leu Ser Leu Pro His Tyr Asn Val Ile Glu
                35   40   45

Arg Val Asn Trp Met Tyr Phe Tyr Glu Tyr Glu Pro Ile Tyr Arg
                50   55   60

Gln Asp Phe His Phe Thr Leu Arg Glu His Ser Asn Cys Ser His
                65   70   75

Gln Asn Pro Phe Leu Val Ile Leu Val Thr Ser His Pro Ser Asp
                80   85   90

Val Lys Ala Arg Gln Ala Ile Arg Val Thr Trp Gly Glu Lys Lys
                95   100   105

Ser Trp Trp Gly Tyr Glu Val Leu Thr Phe Phe Leu Leu Gly Gln
               110   115   120

Glu Ala Glu Lys Glu Asp Lys Met Leu Ala Leu Ser Leu Glu Asp
               125   130   135

Glu His Leu Leu Tyr Gly Asp Ile Ile Arg Gln Asp Phe Leu Asp
               140   145   150

Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile Met Ala Phe Arg Trp
               155   160   165

Val Thr Glu Phe Cys Pro Asn Ala Lys Tyr Val Met Lys Thr Asp
               170   175   180

Thr Asp Val Phe Ile Asn Thr Gly Asn Leu Val Lys Tyr Leu Leu
               185   190   195

Asn Leu Asn His Ser Glu Lys Phe Phe Thr Gly Tyr Pro Leu Ile
               200   205   210

Asp Asn Tyr Ser Tyr Arg Gly Phe Tyr Gln Lys Thr His Ile Ser
               215   220   225

Tyr Gln Glu Tyr Pro Phe Lys Val Phe Pro Pro Tyr Cys Ser Gly
               230   235   240

Leu Gly Tyr Ile Met Ser Arg Asp Leu Val Pro Arg Ile Tyr Glu
               245   250   255

Met Met Gly His Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val

200

Gly Ile Cys Leu Asn Leu Leu Lys Val Asn Ile His Ile Pro Glu
                275   280   285

Asp Thr Asn Leu Phe Phe Leu Tyr Arg Ile His Leu Asp Val Cys
                290   295   300

Gln Leu Arg Arg Val Ile Ala Ala His Gly Phe Ser Ser Lys Glu
                305   310   315

Ile Ile Thr Phe Trp Gln Val Met Leu Arg Asn Thr Thr Cys His
                320   325   330

Tyr

<210> 210
<211> 745
<212> DNA
<213> Homo sapiens

<400> 210
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 caacgtcaat gatgacaaca caatgctgg aagtgggcag cagtcagtga 150

 gtgtcaacaa tgaacacaat gtggccaatg ttgacaataa caacggatgg 200

 gactcctgga attccatctg ggattatgga aatggctttg ctgcaaccag 250

 actctttcaa aagaagacat gcattgtgca caaaatgaac aaggaagtca 300

 tgccctccat tcaatccctt gatgcactgg tcaaggaaaa gaagcttcag 350

 ggtaaggggac caggaggacc acctcccaag ggcctgatgt actcagtcaa 400

 cccaaacaaa gtcgatgacc tgagcaagtt cggaaaaaac attgcaaaca 450

 tgtgtcgtgg gattccaaca tacatggctg aggagatgca agaggcaagc 500

 ctgttttttt actcaggaac gtgctacacg accagtgtac tatggattgt 550

 ggacatttcc ttctgtggag acacggtgga gaactaaaca atttttaaa 600

 gccactatgg atttagtcat ctgaatatgc tgtgcagaaa aaatatgggc 650

 tccagtggtt tttaccatgt cattctgaaa tttttctcta ctagttatgt 700

 ttgatttctt taagtttcaa taaaatcatt tagcattgaa aaaaa 745

<210> 211
<211> 185
<212> PRT
<213> Homo sapiens

<400> 211

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Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu
 1               5                  10                      15

Ala Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn
                20                  25                      30

Asn Asn Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu
                35                  40                      45

His Asn Val Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp
                50                  55                      60

Asn Ser Ile Trp Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu
                65                  70                      75

Phe Gln Lys Lys Thr Cys Ile Val His Lys Met Asn Lys Glu Val
                80                  85                      90

Met Pro Ser Ile Gln Ser Leu Asp Ala Leu Val Lys Glu Lys Lys
                95                 100                     105

Leu Gln Gly Lys Gly Pro Gly Gly Pro Pro Lys Gly Leu Met
               110                 115                     120

Tyr Ser Val Asn Pro Asn Lys Val Asp Asp Leu Ser Lys Phe Gly
               125                 130                     135

Lys Asn Ile Ala Asn Met Cys Arg Gly Ile Pro Thr Tyr Met Ala
               140                 145                     150

Glu Glu Met Gln Glu Ala Ser Leu Phe Phe Tyr Ser Gly Thr Cys
               155                 160                     165

Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile Ser Phe Cys Gly
               170                 175                     180

Asp Thr Val Glu Asn
               185
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<210> 212
<211> 1706
<212> DNA
<213> Homo sapiens

<400> 212

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tacagaagta tattaacttt ttaggagtaa tttctagttt ggattgtaat 100

atgaaataat ttaaaagggc ttcgctcata tataggaaaa tcgcatatgg 150

tcctagtatt aaattcttat tgcttactga tttttttgag ttaagagttg 200

ttatatgcta gaatatgagg atgtgaatat aaataagaga agaaaaaaga 250

ataaagtaga ttgagtctcc aattttatgt aagcttcaga agaactggtt 300
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202

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tgtttacatg caagcttata gttgaaatat ttttcaggaa ttacatgaat 350

gacagtcttc gaaccaatgt gtttgttcga tttcaaccag agactatagc 400

atgtgcttgc atctaccttg cagctagagc acttcagatt ccgttgccaa 450

ctcgtcccca ttggtttctt cttttggta ctacagaaga ggaaatccag 500

gaaatctgca tagaaacact taggctttat accagaaaaa agccaaacta 550

tgaattactg gaaaagaag tagaaaaaag aaaagtagcc ttacaagaag 600

ccaaattaaa agcaaaggga ttgaatccgg atggaactcc agccctttca 650

accctgggtg gattttctcc agcctccaag ccatcatcac caagagaagt 700

aaaagctgaa gagaaatcac caatctccat taatgtgaag acagtcaaaa 750

aagaacctga ggatagacaa caggcttcca aaagcccttca caatggtgta 800

agaaaagaca gcaagagaag tagaaatagc agaagtgcaa gtcgatcgag 850

gtcaagaaca cgatcacgtt ctagatcaca tactccaaga agacactata 900

ataataggcg gagtcgatct ggaacataca gctcgagatc aagaagcagg 950

tcccgcagtc acagtgaaag ccctcgaaga catcataatc atggttctcc 1000

tcaccttaag gccaagcata ccagagatga tttaaaaagt tcaaacagac 1050

atggtcataa aaggaaaaaa tctcgttctc gatctcagag caagtctcgg 1100

gatcactcag atgcagccaa gaaacacagg catgaaaggg gacatcatag 1150

ggacaggcgt gaacgatctc gctcctttga gaggtcccat aaaagcaagc 1200

accatggtgg cagtcgctca ggacatggca ggcacaggcg ctgactttct 1250

cttcctttga gcctgcatca gttcttggtt ttgcctatct acagtgtgat 1300

gtatggactc aatcaaaaac attaaacgca aactgattag gatttgattt 1350

cttgaaaccc tctaggtctc tagaacactg aggacagttt cttttgaaaa 1400

gaactatgtt aattttttg cacattaaaa tgccctagca gtatctaatt 1450

aaaaaccatg gtcaggttca attgtacttt attatagttg tgtattgttt 1500

attgctataa gaactggagc gtgaattctg taaaaatgta tcttattttt 1550

atacagataa aattgcagac actgttctat ttaagtggtt atttgtttaa 1600

atgatggtga atactttctt aacactggtt tgtctgcatg tgtaaagatt 1650

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aaaagt 1706
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203

<210> 213
<211> 299
<212> PRT
<213> Homo sapiens

<400> 213
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Met Asn Asp Ser Leu Arg Thr Asn Val Phe Val Arg Phe Gln Pro
  1               5                  10                  15

Glu Thr Ile Ala Cys Ala Cys Ile Tyr Leu Ala Ala Arg Ala Leu
               20                  25                  30

Gln Ile Pro Leu Pro Thr Arg Pro His Trp Phe Leu Leu Phe Gly
               35                  40                  45

Thr Thr Glu Glu Glu Ile Gln Glu Ile Cys Ile Glu Thr Leu Arg
               50                  55                  60

Leu Tyr Thr Arg Lys Lys Pro Asn Tyr Glu Leu Leu Glu Lys Glu
               65                  70                  75

Val Glu Lys Arg Lys Val Ala Leu Gln Glu Ala Lys Leu Lys Ala
               80                  85                  90

Lys Gly Leu Asn Pro Asp Gly Thr Pro Ala Leu Ser Thr Leu Gly
               95                 100                 105

Gly Phe Ser Pro Ala Ser Lys Pro Ser Ser Pro Arg Glu Val Lys
              110                 115                 120

Ala Glu Glu Lys Ser Pro Ile Ser Ile Asn Val Lys Thr Val Lys
              125                 130                 135

Lys Glu Pro Glu Asp Arg Gln Gln Ala Ser Lys Ser Pro Tyr Asn
              140                 145                 150

Gly Val Arg Lys Asp Ser Lys Arg Ser Arg Asn Ser Arg Ser Ala
              155                 160                 165

Ser Arg Ser Arg Ser Arg Thr Arg Ser Arg Ser Arg Ser His Thr
              170                 175                 180

Pro Arg Arg His Tyr Asn Asn Arg Arg Ser Arg Ser Gly Thr Tyr
              185                 190                 195

Ser Ser Arg Ser Arg Ser Arg Ser Arg Ser His Ser Glu Ser Pro
              200                 205                 210

Arg Arg His His Asn His Gly Ser Pro His Leu Lys Ala Lys His
              215                 220                 225

Thr Arg Asp Asp Leu Lys Ser Ser Asn Arg His Gly His Lys Arg
              230                 235                 240

Lys Lys Ser Arg Ser Arg Ser Gln Ser Lys Ser Arg Asp His Ser
              245                 250                 255

Asp Ala Ala Lys Lys His Arg His Glu Arg Gly His His Arg Asp
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Arg Arg Glu Arg Ser Arg Ser Phe Glu Arg Ser His Lys Ser Lys
            275   280   285

His His Gly Gly Ser Arg Ser Gly His Gly Arg His Arg Arg
            290   295

<210> 214
<211> 730
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 72-73, 85, 91, 127, 226, 268, 454, 484, 513, 566, 663
<223> unknown base

<400> 214
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gcattgcttt ttacagaaat atattanctt tttagagtaa tttctagttt 150

ggattgtaat atgaaattat ttaaaagggc ttcgctcata tataggaaaa 200

tcgcatatgg tcctagtatt aaattnttat tgcttactga tttttttgag 250

ttaagagttg ttatatgnta gaatatgagg atgtgaatat aaataagaga 300

agaaaaaaga ataaagtaga ttgagtctcc aattttatgt aagcttcaga 350

agaactggtt tgtttacatg caagcttata gttgaaatat ttttcaggaa 400

ttacatgaat gacagtcttc gaaccaatgt gtttgttcga tttcaaccag 450

agantatagc atgtgcttgc atctaccttg cagntagagc acttcagatt 500

ccgttgccaa ctngtcccca ttggtttctt cttttttggta ctacagaaga 550

ggaaatccag gaaatntgca tagaaacact taggctttat accagaaaaa 600

agccaaacta tgaattactg gaaaaagaag tagaaaaaag aaaagtagcc 650

ttacaagaag ccnaattaaa agcaaaggga ttgaatccgg atggaactcc 700

agcccttttca accctgggtg gattttctcc 730

<210> 215
<211> 1807
<212> DNA
<213> Homo sapiens

<400> 215
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acgcgtcatg gcggtcctcg gagtacagct ggtggtgacc ctgctcactg 100

205

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ccaccctcat gcacaggctg gcgccacact gctccttcgc gcgctggctg 150

ctctgtaacg gcagtttgtt ccgatacaag cacccgtctg aggaggagct 200

tcgggccctg gcggggaagc cgaggcccag aggcaggaaa gagcggtggg 250

ccaatggcct tagtgaggag aagccactgt ctgtgccccg agatgccccg 300

ttccagctgg agacctgccc cctcacgacc gtggatgccc tggtcctgcg 350

cttcttcctg gagtaccagt ggtttgtgga ctttgctgtg tactcgggcg 400

gcgtgtacct cttcacagag gcctactact acatgctggg accagccaag 450

gagactaaca ttgctgtgtt ctggtgcctg ctcacggtga ccttctccat 500

caagatgttc ctgacagtga cacggctgta cttcagcgcc gaggaggggg 550

gtgagcgctc tgtctgcctc acctttgcct tcctcttcct gctgctggcc 600

atgctggtgc aagtggtgcg ggaggagacc ctcgagctgg gcctggagcc 650

tggtctggcc agcatgaccc agaacttaga gccacttctg aagaagcagg 700

gctgggactg ggcgcttcct gtggccaagc tggctatccg cgtgggactg 750

gcagtggtgg gctctgtgct gggtgccttc ctcaccttcc caggcctgcg 800

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gcgaagggag gctggccgca tcgaagcccg tgaaatccag cagagggtgg 1150

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cctgcagacc ctcctggggc cctgaggtct gttcctgggg cagcgggaca 1550
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206

ctagcctgcc ccctctgttt gcgcccccgt gtccccagct gcaaggtggg 1600

gccggactcc ccggcgttcc cttcaccaca gtgcctgacc cgcggccccc 1650

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ggcgagggtg atgctggctg ctcttctgaa caaataaagg agcatgccga 1800

tttttaa 1807

<210> 216
<211> 479
<212> PRT
<213> Homo sapiens

<400> 216
Met Ala Val Leu Gly Val Gln Leu Val Val Thr Leu Leu Thr Ala
 1   5   10   15

Thr Leu Met His Arg Leu Ala Pro His Cys Ser Phe Ala Arg Trp
                20   25   30

Leu Leu Cys Asn Gly Ser Leu Phe Arg Tyr Lys His Pro Ser Glu
                35   40   45

Glu Glu Leu Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg
                50   55   60

Lys Glu Arg Trp Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser
                65   70   75

Val Pro Arg Asp Ala Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr
                80   85   90

Thr Val Asp Ala Leu Val Leu Arg Phe Phe Leu Glu Tyr Gln Trp
                95   100   105

Phe Val Asp Phe Ala Val Tyr Ser Gly Gly Val Tyr Leu Phe Thr
                110   115   120

Glu Ala Tyr Tyr Tyr Met Leu Gly Pro Ala Lys Glu Thr Asn Ile
                125   130   135

Ala Val Phe Trp Cys Leu Leu Thr Val Thr Phe Ser Ile Lys Met
                140   145   150

Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser Ala Glu Glu Gly Gly
                155   160   165

Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu Phe Leu Leu Leu
                170   175   180

Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu Glu Leu Gly
                185   190   195

Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu Pro Leu

207

                    200   205   210

Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys Leu
                215   220   225

Ala Ile Arg Val Gly Leu Ala Val Val Gly Ser Val Leu Gly Ala
                230   235   240

Phe Leu Thr Phe Pro Gly Leu Arg Leu Ala Gln Thr His Arg Asp
                245   250   255

Ala Leu Thr Met Ser Glu Asp Arg Pro Met Leu Gln Phe Leu Leu
                260   265   270

His Thr Ser Phe Leu Ser Pro Leu Phe Ile Leu Trp Leu Trp Thr
                275   280   285

Lys Pro Ile Ala Arg Asp Phe Leu His Gln Pro Pro Phe Gly Glu
                290   295   300

Thr Arg Phe Ser Leu Leu Ser Asp Ser Ala Phe Asp Ser Gly Arg
                305   310   315

Leu Trp Leu Leu Val Val Leu Cys Leu Leu Arg Leu Ala Val Thr
                320   325   330

Arg Pro His Leu Gln Ala Tyr Leu Cys Leu Ala Lys Ala Arg Val
                335   340   345

Glu Gln Leu Arg Arg Glu Ala Gly Arg Ile Glu Ala Arg Glu Ile
                350   355   360

Gln Gln Arg Val Val Arg Val Tyr Cys Tyr Val Thr Val Val Ser
                365   370   375

Leu Gln Tyr Leu Thr Pro Leu Ile Leu Thr Leu Asn Cys Thr Leu
                380   385   390

Leu Leu Lys Thr Leu Gly Gly Tyr Ser Trp Gly Leu Gly Pro Ala
                395   400   405

Pro Leu Leu Ser Pro Asp Pro Ser Ser Ala Ser Ala Ala Pro Ile
                410   415   420

Gly Ser Gly Glu Asp Glu Val Gln Gln Thr Ala Ala Arg Ile Ala
                425   430   435

Gly Ala Leu Gly Gly Leu Leu Thr Pro Leu Phe Leu Arg Gly Val
                440   445   450

Leu Ala Tyr Leu Ile Trp Trp Thr Ala Ala Cys Gln Leu Leu Ala
                455   460   465

Ser Leu Phe Gly Leu Tyr Phe His Gln His Leu Ala Gly Ser
                470   475

<210> 217
<211> 574

208

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 5, 146
<223> unknown base

<400> 217
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gctggctgct ctgtaacggc agtttgttcc gatacaagca cccgtnttga 150

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agcggtgggc caatggcctt agtgaggaga agccactgtc tgtgccccga 250

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ggtcctgcgc ttcttcctgg agtaccagtg gtttgtggac tttgctgtgt 350

actcgggcgg cgtgtacctc ttcacagagg cctactacta catgctggga 400

ccagccaagg agactaacat tgctgtgttc tggtgcctgc tcacagtgac 450

cttctccatc aagatgttcc tgacagtgac acggctgtac ttcagcgccg 500

aggaggggg tgagcgctct gtctgcctca cctttgcctt cctcttcctg 550

ctgctggcca tgctggtgca agcg 574
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<210> 218
<211> 2571
<212> DNA
<213> Homo sapiens

<400> 218
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ttgtgatcta ctgattgtgg gggcatggca aggtttgctt aaaggagctt 150

ggctggtttg ggcccttgta gctgacagaa ggtggccagg gagaatgcag 200

cacactgctc ggagaatgaa ggcgcttctg ttgctggtct tgccttggct 250

cagtcctgct aactacattg acaatgtggg caacctgcac ttcctgtatt 300

cagaactctg taaaggtgcc tcccactacg gcctgaccaa agataggaag 350

aggcgctcac aagatggctg tccagacggc tgtgcgagcc tcacagccac 400

ggctccctcc ccagaggttt ctgcagctgc caccatctcc ttaatgacag 450

acgagcctgg cctagacaac cctgcctacg tgtcctcggc agaggacggg 500
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209

cagccagcaa tcagcccagt ggactctggc cggagcaacc gaactagggc 550

acggcccttt gagagatcca ctattagaag cagatcattt aaaaaaataa 600

atcgagcttt gagtgttctt cgaaggacaa agagcgggag tgcagttgcc 650

aaccatgccg accagggcag ggaaaattct gaaaacacca ctgcccctga 700

agtctttcca aggttgtacc acctgattcc agatggtgaa attaccagca 750

tcaagatcaa tcgagtagat cccagtgaaa gcctctctat taggctggtg 800

ggaggtagcg aaaccccact ggtccatatc attatccaac acatttatcg 850

tgatggggtg atcgccagag acggccggct actgccagga gacatcattc 900

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ccagaaagtg cggctcatct gattcaggcc agtgaaagac gtgttcacct 1300

cgtcgtgtcc cgccaggttc ggcagcggag ccctgacatc tttcaggaag 1350

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cccggaggag tcataagcag agatggaaga ataaaaacag gtgacatttt 1600

gttgaatgtg gatggggtcg aactgacaga ggtcagccgg agtgaggcag 1650

tggcattatt gaaaagaaca tcatcctcga tagtactcaa agctttggaa 1700

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tgtggctgga attaccacgg tgcttgtata actgtaaaga tattgtatta 1850

cgaagaaaca cagctggaag tctgggcttc tgcattgtag gaggttatga 1900

agaatacaat ggaaacaaac ctttttttcat caaatccatt gttgaaggaa 1950

210

caccagcata caatgatgga agaattagat gtggtgatat tcttcttgct 2000

gtcaatggta gaagtacatc aggaatgata catgcttgct tggcaagact 2050

gctgaaagaa cttaaaggaa gaattactct aactattgtt tcttggcctg 2100

gcactttttt atagaatcaa tgatgggtca gaggaaaaca gaaaaatcac 2150

aaataggcta agaagttgaa acactatatt tatcttgtca gtttttatat 2200

ttaaagaaag aatacattgt aaaaatgtca ggaaaagtat gatcatctaa 2250

tgaaagccag ttacacctca gaaatatga ttccaaaaaa attaaaacta 2300

ctagtttttt ttcagtgtgg aggatttctc attactctac aacattgttt 2350

atattttttc tattcaataa aaagccctaa aacaactaaa atgattgatt 2400

tgtataccc actgaattca agctgattta aatttaaaat ttggtatatg 2450

ctgaagtctg ccaagggtac attatggcca ttttaatt acagctaaaa 2500

tatttttaa aatgcattgc tgagaaacgt tgctttcatc aaacaagaat 2550

aaatatttt cagaagttaa a 2571

<210> 219
<211> 632
<212> PRT
<213> Homo sapiens

<400> 219
Met Lys Ala Leu Leu Leu Val Leu Pro Trp Leu Ser Pro Ala
 1   5   10   15

Asn Tyr Ile Asp Asn Val Gly Asn Leu His Phe Leu Tyr Ser Glu
                 20   25   30

Leu Cys Lys Gly Ala Ser His Tyr Gly Leu Thr Lys Asp Arg Lys
                 35   40   45

Arg Arg Ser Gln Asp Gly Cys Pro Asp Gly Cys Ala Ser Leu Thr
                 50   55   60

Ala Thr Ala Pro Ser Pro Glu Val Ser Ala Ala Thr Ile Ser
                 65   70   75

Leu Met Thr Asp Glu Pro Gly Leu Asp Asn Pro Ala Tyr Val Ser
                 80   85   90

Ser Ala Glu Asp Gly Gln Pro Ala Ile Ser Pro Val Asp Ser Gly
                 95   100   105

Arg Ser Asn Arg Thr Arg Ala Arg Pro Phe Glu Arg Ser Thr Ile
                 110   115   120

Arg Ser Arg Ser Phe Lys Lys Ile Asn Arg Ala Leu Ser Val Leu
                 125   130   135

211

Arg Arg Thr Lys Ser Gly Ser Ala Val Ala Asn His Ala Asp Gln
            140   145   150

Gly Arg Glu Asn Ser Glu Asn Thr Thr Ala Pro Glu Val Phe Pro
            155   160   165

Arg Leu Tyr His Leu Ile Pro Asp Gly Glu Ile Thr Ser Ile Lys
            170   175   180

Ile Asn Arg Val Asp Pro Ser Glu Ser Leu Ser Ile Arg Leu Val
            185   190   195

Gly Gly Ser Glu Thr Pro Leu Val His Ile Ile Ile Gln His Ile
            200   205   210

Tyr Arg Asp Gly Val Ile Ala Arg Asp Gly Arg Leu Leu Pro Gly
            215   220   225

Asp Ile Ile Leu Lys Val Asn Gly Met Asp Ile Ser Asn Val Pro
            230   235   240

His Asn Tyr Ala Val Arg Leu Leu Arg Gln Pro Cys Gln Val Leu
            245   250   255

Trp Leu Thr Val Met Arg Glu Gln Lys Phe Arg Ser Arg Asn Asn
            260   265   270

Gly Gln Ala Pro Asp Ala Tyr Arg Pro Arg Asp Asp Ser Phe His
            275   280   285

Val Ile Leu Asn Lys Ser Ser Pro Glu Glu Gln Leu Gly Ile Lys
            290   295   300

Leu Val Arg Lys Val Asp Glu Pro Gly Val Phe Ile Phe Asn Val
            305   310   315

Leu Asp Gly Gly Val Ala Tyr Arg His Gly Gln Leu Glu Glu Asn
            320   325   330

Asp Arg Val Leu Ala Ile Asn Gly His Asp Leu Arg Tyr Gly Ser
            335   340   345

Pro Glu Ser Ala Ala His Leu Ile Gln Ala Ser Glu Arg Arg Val
            350   355   360

His Leu Val Val Ser Arg Gln Val Arg Gln Arg Ser Pro Asp Ile
            365   370   375

Phe Gln Glu Ala Gly Trp Asn Ser Asn Gly Ser Trp Ser Pro Gly
            380   385   390

Pro Gly Glu Arg Ser Asn Thr Pro Lys Pro Leu His Pro Thr Ile
            395   400   405

Thr Cys His Glu Lys Val Val Asn Ile Gln Lys Asp Pro Gly Glu
            410   415   420

Ser Leu Gly Met Thr Val Ala Gly Gly Ala Ser His Arg Glu Trp

212

Asp Leu Pro Ile Tyr Val Ile Ser Val Glu Pro Gly Gly Val Ile
            440   445   450

Ser Arg Asp Gly Arg Ile Lys Thr Gly Asp Ile Leu Leu Asn Val
            455   460   465

Asp Gly Val Glu Leu Thr Glu Val Ser Arg Ser Glu Ala Val Ala
            470   475   480

Leu Leu Lys Arg Thr Ser Ser Ser Ile Val Leu Lys Ala Leu Glu
            485   490   495

Val Lys Glu Tyr Glu Pro Gln Glu Asp Cys Ser Ser Pro Ala Ala
            500   505   510

Leu Asp Ser Asn His Asn Met Ala Pro Pro Ser Asp Trp Ser Pro
            515   520   525

Ser Trp Val Met Trp Leu Glu Leu Pro Arg Cys Leu Tyr Asn Cys
            530   535   540

Lys Asp Ile Val Leu Arg Arg Asn Thr Ala Gly Ser Leu Gly Phe
            545   550   555

Cys Ile Val Gly Gly Tyr Glu Glu Tyr Asn Gly Asn Lys Pro Phe
            560   565   570

Phe Ile Lys Ser Ile Val Glu Gly Thr Pro Ala Tyr Asn Asp Gly
            575   580   585

Arg Ile Arg Cys Gly Asp Ile Leu Leu Ala Val Asn Gly Arg Ser
            590   595   600

Thr Ser Gly Met Ile His Ala Cys Leu Ala Arg Leu Leu Lys Glu
            605   610   615

Leu Lys Gly Arg Ile Thr Leu Thr Ile Val Ser Trp Pro Gly Thr
            620   625   630

Phe Leu

<210> 220
<211> 773
<212> DNA
<213> Homo sapiens

<400> 220
 ccaaagtgat catttgaaaa agagatatcc acatcttcaa gcccatataa 50

 aggatagaag ctgcacaggg cagctttact tactccagca ccttcctctc 100

 ccaggcaaat ggtgctgacc atctttggga tacaatctca tggatacgag 150

 gtttttaaca tcatcagccc aagcaacaat ggtggcaatg ttcaggagac 200

agtgacaatt gataatgaaa aaaataccgc catcgttaac atccatgcag 250

gatcatgctc ttctaccaca atttttgact ataaacatgg ctacattgca 300

tccagggtgc tctcccgaag agcctgcttt atcctgaaga tggaccatca 350

gaacatccct cctctgaaca atctccaatg gtacatctat gagaaacagg 400

ctctggacaa catgttctcc aacaaataca cctgggtcaa gtacaaccct 450

ctggagtctc tgatcaaaga cgtggattgg ttcctgcttg ggtcacccat 500

tgagaaactc tgcaaacata tccctttgta taggggggaa gtggttgaaa 550

acacacataa tgtcggtgct ggaggctgtg caaaggctgg gctcctgggc 600

atcttgggaa tttcaatctg tgcagacatt catgtttagg atgattagcc 650

ctcttgtttt atcttttcaa agaaatacat ccttggttta cactcaaaag 700

tcaaattaaa ttctttccca atgccccaac taattttgag attcagtcag 750

aaaatataaa tgctgtattt ata 773

<210> 221
<211> 184
<212> PRT
<213> Homo sapiens

<400> 221
Met Lys Ile Leu Val Ala Phe Leu Val Val Leu Thr Ile Phe Gly
  1   5   10   15

Ile Gln Ser His Gly Tyr Glu Val Phe Asn Ile Ile Ser Pro Ser
                 20   25   30

Asn Asn Gly Gly Asn Val Gln Glu Thr Val Thr Ile Asp Asn Glu
                 35   40   45

Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser
                 50   55   60

Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val
                 65   70   75

Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn
                 80   85   90

Ile Pro Pro Leu Asn Asn Leu Gln Trp Tyr Ile Tyr Glu Lys Gln
                 95   100   105

Ala Leu Asp Asn Met Phe Ser Asn Lys Tyr Thr Trp Val Lys Tyr
                110   115   120

Asn Pro Leu Glu Ser Leu Ile Lys Asp Val Asp Trp Phe Leu Leu
                125   130   135

Gly Ser Pro Ile Glu Lys Leu Cys Lys His Ile Pro Leu Tyr Lys

214

Gly Glu Val Val Glu Asn Thr His Asn Val Gly Ala Gly Gly Cys
                    155   160   165

Ala Lys Ala Gly Leu Leu Gly Ile Leu Gly Ile Ser Ile Cys Ala
                170   175   180

Asp Ile His Val

<210> 222
<211> 992
<212> DNA
<213> Homo sapiens

<400> 222
 ggcacgagcc aggaactagg aggttctcac tgcccgagca gaggccctac 50

 acccaccgag gcatggggct ccctgggctg ttctgcttgg ccgtgctggc 100

 tgccagcagc ttctccaagg cacgggagga agaaattacc cctgtggtct 150

 ccattgccta caaagtcctg gaagttttcc ccaaaggccg ctgggtgctc 200

 ataacctgct gtgcacccca gccaccaccg cccatcacct attccctctg 250

 tggaaccaag aacatcaagg tggccaagaa ggtggtgaag acccacgagc 300

 cggcctcctt caacctcaac gtcacactca gtccagtcc agacctgctc 350

 acctacttct gccgggcgtc ctccacctca ggtgcccatg tggacagtgc 400

 caggctacag atgcactggg agctgtggtc caagccagtg tctgagctgc 450

 gggccaactt cactctgcag gacagagggg caggccccag ggtggagatg 500

 atctgccagg cgtcctcggg cagcccacct atcaccaaca gcctgatcgg 550

 gaaggatggg caggtccacc tgcagcagag accatgccac aggcagcctg 600

 ccaacttctc cttcctgccg agccagacat cggactggtt ctggtgccag 650

 gctgcaaaca cgccaatgt ccagcacagc gccctcacag tggtgccccc 700

 aggtggtgac cagaagatgg aggactggca gggtcccctg gagagcccca 750

 tccttgcctt gccgctctac aggagcaccc gccgtctgag tgaagaggag 800

 tttgggggggt tcaggatagg gaatggggag gtcagaggac gcaaagcagc 850

 agccatgtag aatgaaccgt ccagagagcc aagcacggca gaggactgca 900

 ggccatcagc gtgcactgtt cgtatttgga gttcatgcaa aatgagtgtg 950

 ttttagctgc tcttgccaca aaaaaaaaaa aaaaaaaaaa aa 992

<210> 223

<211> 265
<212> PRT
<213> Homo sapiens

<400> 223
Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser
1   5   10   15

Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser
                20   25   30

Ile Ala Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val
                35   40   45

Leu Ile Thr Cys Cys Ala Pro Gln Pro Pro Pro Ile Thr Tyr
                50   55   60

Ser Leu Cys Gly Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val
                65   70   75

Lys Thr His Glu Pro Ala Ser Phe Asn Leu Asn Val Thr Leu Lys
                80   85   90

Ser Ser Pro Asp Leu Leu Thr Tyr Phe Cys Arg Ala Ser Ser Thr
                95   100   105

Ser Gly Ala His Val Asp Ser Ala Arg Leu Gln Met His Trp Glu
                110   115   120

Leu Trp Ser Lys Pro Val Ser Glu Leu Arg Ala Asn Phe Thr Leu
                125   130   135

Gln Asp Arg Gly Ala Gly Pro Arg Val Glu Met Ile Cys Gln Ala
                140   145   150

Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser Leu Ile Gly Lys Asp
                155   160   165

Gly Gln Val His Leu Gln Gln Arg Pro Cys His Arg Gln Pro Ala
                170   175   180

Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp Phe Trp Cys
                185   190   195

Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu Thr Val
                200   205   210

Val Pro Pro Gly Gly Asp Gln Lys Met Glu Asp Trp Gln Gly Pro
                215   220   225

Leu Glu Ser Pro Ile Leu Ala Leu Pro Leu Tyr Arg Ser Thr Arg
                230   235   240

Arg Leu Ser Glu Glu Glu Phe Gly Gly Phe Arg Ile Gly Asn Gly
                245   250   255

Glu Val Arg Gly Arg Lys Ala Ala Ala Met
                260   265

<210> 224
<211> 1297
<212> DNA
<213> Homo sapiens

<400> 224
ggtccttaat ggcagcagcc gccgctacca agatccttct gtgcctcccg 50

cttctgctcc tgctgtccgg ctggtcccgg gctgggcgag ccgaccctca 100

ctctctttgc tatgacatca ccgtcatccc taagttcaga cctggaccac 150

ggtggtgtgc ggttcaaggc caggtggatg aaaagacttt tcttcactat 200

gactgtggca acaagacagt cacacctgtc agtcccctgg ggaagaaact 250

aaatgtcaca acggcctgga aagcacagaa cccagtactg agagaggtgg 300

tggacatact tacagagcaa ctgcgtgaca ttcagctgga gaattacaca 350

cccaaggaac ccctcaccct gcaggcaagg atgtcttgtg agcagaaagc 400

tgaaggacac agcagtggat cttggcagtt cagtttcgat gggcagatct 450

tcctcctctt tgactcagag aagagaatgt ggacaacggt tcatcctgga 500

gccagaaaga tgaaagaaaa gtgggagaat gacaaggttg tggccatgtc 550

cttccattac ttctcaatgg gagactgtat aggatggctt gaggacttct 600

tgatgggcat ggacagcacc ctggagccaa gtgcaggagc accactcgcc 650

atgtcctcag gcacaaccca actcagggcc acagccacca ccctcatcct 700

ttgctgcctc ctcatcatcc tcccctgctt catcctccct ggcatctgag 750

gagagtcctt tagagtgaca ggttaaagct gataccaaaa ggctcctgtg 800

agcacggtct tgatcaaact cgcccttctg tctggccagc tgcccacgac 850

ctacggtgta tgtccagtgg cctccagcag atcatgatga catcatggac 900

ccaatagctc attcactgcc ttgattcctt ttgccaacaa ttttaccagc 950

agttatacct aacatattat gcaattttct cttggtgcta cctgatggaa 1000

ttcctgcact taaagttctg gctgactaaa caagatatat cattttcttt 1050

cttctctttt tgtttggaaa atcaagtact tctttgaatg atgatctctt 1100

tcttgcaaat gatattgtca gtaaaataat cacgttagac ttcagacctc 1150

tggggattct ttccgtgtcc tgaaagagaa tttttaaatt atttaataag 1200

aaaaaattta tattaatgat tgtttccttt agtaatttat tgttctgtac 1250

tgatatttaa ataaagagtt ctatttccca aaaaaaaaaa aaaaaaa 1297

217

<210> 225
<211> 246
<212> PRT
<213> Homo sapiens

<400> 225
Met Ala Ala Ala Ala Ala Thr Lys Ile Leu Leu Cys Leu Pro Leu
 1   5   10   15

Leu Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro
                20   25   30

His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro
                35   40   45

Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
                50   55   60

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser
                65   70   75

Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln
                80   85   90

Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
                95   100   105

Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr
                110   115   120

Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser
                125   130   135

Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu
                140   145   150

Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala
                155   160   165

Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met
                170   175   180

Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu
                185   190   195

Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala Gly
                200   205   210

Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala Thr
                215   220   225

Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys
                230   235   240

Phe Ile Leu Pro Gly Ile
                245

<210> 226

218

<211> 735
<212> DNA
<213> Homo sapiens

<400> 226
 gggaaagcca tttcgaaaac ccatctatac aaactatata ttttcatttc 50

 tgctgctagc tgccttgggc ctcacaattt tcattctgtt ttctgacttt 100

 caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

 ggttttaatt ttggtggtag ccctcaccca attctggtgt ggctttcttt 200

 gcagaggatt ccaccttcaa aatcatgaac tctggctgtt gatcaaaaga 250

 gaatttggat tctactctaa aagtcaatat aggacttggc aaaagaagct 300

 agcagaagac tcaacctggc ctcccataaa caggacagat tattcaggtg 350

 atggcaaaaa tggattctac atcaacggag gctatgaaag ccatgaacag 400

 attccaaaaa gaaaactcaa attgggaggc caacccacag aacagcattt 450

 ctgggccagg ctgtaatcag aattgtcgtc gtacatgctc aacagcattg 500

 cttttttccc caaaattaac acattgtgga gaagtgatga tactctcccc 550

 ttaccttcc tctctccatt caagcattca aagtatattt tcaatgaatt 600

 aaaccttgca gcaagggacc ttagataggc ttattctgac tgtatgcttt 650

 accaatgaga gaaaaaaatg catttcctgt atcatccttt tcaataaact 700

 gtattcattt tgaaaaaaaa aaaaaaaaaa aaaaa 735

<210> 227
<211> 115
<212> PRT
<213> Homo sapiens

<400> 227
 Met Glu Leu Ile Pro Thr Ile Thr Ser Trp Arg Val Leu Ile Leu
  1   5   10   15

 Val Val Ala Leu Thr Gln Phe Trp Cys Gly Phe Leu Cys Arg Gly
                 20   25   30

 Phe His Leu Gln Asn His Glu Leu Trp Leu Leu Ile Lys Arg Glu
                 35   40   45

 Phe Gly Phe Tyr Ser Lys Ser Gln Tyr Arg Thr Trp Gln Lys Lys
                 50   55   60

 Leu Ala Glu Asp Ser Thr Trp Pro Pro Ile Asn Arg Thr Asp Tyr
                 65   70   75

 Ser Gly Asp Gly Lys Asn Gly Phe Tyr Ile Asn Gly Gly Tyr Glu
                 80   85   90

219

```
Ser His Glu Gln Ile Pro Lys Arg Lys Leu Lys Leu Gly Gly Gln
              95                  100                 105

Pro Thr Glu Gln His Phe Trp Ala Arg Leu
              110             115
```

<210> 228
<211> 2185
<212> DNA
<213> Homo sapiens

<400> 228

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gttctccttt ccgagccaaa atcccaggcg atggtgaatt atgaacgtgc 50

cacaccatga agctcttgtg gcaggtaact gtgcaccacc acacctggaa 100

tgccatcctg ctcccgttcg tctacctcac ggcgcaagtg tggattctgt 150

gtgcagccat cgctgctgcc gcctcagccg gccccagaa ctgcccctcc 200

gtttgctcgt gcagtaacca gttcagcaag gtggtgtgca cgcgccgggg 250

cctctccgag gtcccgcagg gtattccctc gaacacccgg tacctcaacc 300

tcatggagaa caacatccag atgatccagg ccgacacctt ccgccacctc 350

caccacctgg aggtcctgca gttgggcagg aactccatcc ggcagattga 400

ggtggggggcc ttcaacggcc tggccagcct caacaccctg gagctgttcg 450

acaactggct gacagtcatc cctagcgggg cctttgaata cctgtccaag 500

ctgcgggagc tctggcttcg caacaacccc atcgaaagca tcccctctta 550

cgccttcaac cgggtgccct ccctcatgcg cctggacttg ggggagctca 600

agaagctgga gtatatctct gagggagctt ttgaggggct gttcaacctc 650

aagtatctga acttgggcat gtgcaacatt aaagacatgc caatctcac 700

cccctggtg gggctggagg agctggagat gtcaggaac cacttccctg 750

agatcaggcc tggctccttc catggcctga gctccctcaa gaagctctgg 800

gtcatgaact cacaggtcag cctgattgag cggaatgctt ttgacgggct 850

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cccatgacct ctttacccog ctgaggtacc tggtggagtt gcatctacac 950

cacaacctt ggaactgtga ttgtgacatt ctgtggctag cctggtggct 1000

tcgagagtat atacccacca attccacctg ctgtggccgc tgtcatgctc 1050

ccatgcacat gcgaggccgc tacctcgtgg aggtggacca ggcctccttc 1100

cagtgctctg ccccccttcat catggacgca cctcgagacc tcaacatttc 1150
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tgagggtcgg atggcagaac ttaagtgtcg gactccccct atgtcctccg 1200

tgaagtggtt gctgcccaat gggacagtgc tcagccacgc ctcccgccac 1250

ccaaggatct ctgtcctcaa cgacggcacc ttgaactttt cccacgtgct 1300

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gcctgaggac acaacgcgaa agtacaagcc tgttcctacc acgtccactg 1500

gttaccagcc ggcatatacc acctctacca cggtgctcat tcagactacc 1550

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gcagaccagc ctggatgaag tcatgaagac caccaagatc atcattggct 1650

gctttgtggc agtgactctg ctagctgccg ccatgttgat tgtcttctat 1700

aaacttcgta agcggcacca gcagcggagt acagtcacag ccgcccggac 1750

tgttgagata atccaggtgg acgaagacat cccagcagca acatccgcag 1800

cagcaacagc agctccgtcc ggtgtatcag gtgaggggggc agtagtgctg 1850

cccacaattc atgaccatat taactacaac acctacaaac cagcacatgg 1900

ggcccactgg acagaaaaca gcctggggaa ctctctgcac cccacagtca 1950

ccactatctc tgaaccttat ataattcaga cccataccaa ggacaaggta 2000

caggaaactc aaatatgact cccctccccc aaaaaactta taaaatgcaa 2050

tagaatgcac acaaagacag caacttttgt acagagtggg gagagacttt 2100

ttcttgtata tgcttatata ttaagtctat gggctggtta aaaaaaacag 2150

attatattaa aatttaaaga caaaaagtca aaaca 2185
```

<210> 229
<211> 653
<212> PRT
<213> Homo sapiens

<400> 229

```
Met Lys Leu Leu Trp Gln Val Thr Val His His Thr Trp Asn
 1               5              10                  15

Ala Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile
             20              25                  30

Leu Cys Ala Ala Ile Ala Ala Ala Ala Ser Ala Gly Pro Gln Asn
             35              40                  45

Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val
```

221

Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser
                 65   70   75

Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile
                 80   85   90

Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val Leu Gln
                 95   100   105

Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn
                110   115   120

Gly Leu Ala Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Leu
                125   130   135

Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg
                140   145   150

Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr
                155   160   165

Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu
                170   175   180

Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu
                185   190   195

Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp
                200   205   210

Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu Met
                215   220   225

Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly
                230   235   240

Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Gln Val Ser
                245   250   255

Leu Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu
                260   265   270

Leu Asn Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp Leu
                275   280   285

Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn
                290   295   300

Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu Ala Trp Trp Leu
                305   310   315

Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly Arg Cys His
                320   325   330

Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val Asp Gln
                335   340   345

```
Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro Arg
                350                 355             360

Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg
                365                 370             375

Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr
                380                 385             390

Val Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn
                395                 400             405

Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly
                410                 415             420

Val Tyr Thr Cys Met Val Thr Asn Val Ala Gly Asn Ser Asn Ala
                425                 430             435

Ser Ala Tyr Leu Asn Val Ser Thr Ala Glu Leu Asn Thr Ser Asn
                440                 445             450

Tyr Ser Phe Phe Thr Thr Val Thr Val Glu Thr Thr Glu Ile Ser
                455                 460             465

Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val Pro Thr Thr Ser
                470                 475             480

Thr Gly Tyr Gln Pro Ala Tyr Thr Thr Ser Thr Thr Val Leu Ile
                485                 490             495

Gln Thr Thr Arg Val Pro Lys Gln Val Ala Val Pro Ala Thr Asp
                500                 505             510

Thr Thr Asp Lys Met Gln Thr Ser Leu Asp Glu Val Met Lys Thr
                515                 520             525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala
                530                 535             540

Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln
                545                 550             555

Gln Arg Ser Thr Val Thr Ala Ala Arg Thr Val Glu Ile Ile Gln
                560                 565             570

Val Asp Glu Asp Ile Pro Ala Ala Thr Ser Ala Ala Ala Thr Ala
                575                 580             585

Ala Pro Ser Gly Val Ser Gly Glu Gly Ala Val Val Leu Pro Thr
                590                 595             600

Ile His Asp His Ile Asn Tyr Asn Thr Tyr Lys Pro Ala His Gly
                605                 610             615

Ala His Trp Thr Glu Asn Ser Leu Gly Asn Ser Leu His Pro Thr
                620                 625             630

Val Thr Thr Ile Ser Glu Pro Tyr Ile Ile Gln Thr His Thr Lys
```

223

Asp Lys Val Gln Glu Thr Gln Ile
635   640   645
                    650

<210> 230
<211> 2846
<212> DNA
<213> Homo sapiens

<400> 230
cgctcgggca ccagccgcgg caaggatgga gctgggttgc tggacgcagt 50

tggggctcac ttttcttcag ctccttctca tctcgtcctt gccaagagag 100

tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150

tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200

gggaagtcgt gggttatacc atcccttgct gcaggaatga ggagaatgag 250

tgtgactcct gcctgatcca cccaggttgt accatctttg aaaactgcaa 300

gagctgccga aatggctcat gggggggtac cttggatgac ttctatgtga 350

aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc 400

atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450

aagctatccc ctaaatgctc actgtgaatg gaccattcat gctaaacctg 500

ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550

atgtgccagt atgactatgt tgaggttcgt gatggagaca ccgcgatgg 600

ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga 650

gcataggatc ctcactccac gtcctcttcc actccgatgg ctccaagaat 700

tttgacggtt tccatgccat ttatgaggag atcacagcat gctcctcatc 750

cccttgtttc catgacggca cgtgcgtcct tgacaaggct ggatcttaca 800

agtgtgcctg cttggcaggc tatactgggc agcgctgtga aatctcctt 850

gaagaaagaa actgctcaga ccctggggc ccagtcaatg ggtaccagaa 900

aataacaggg ggccctgggc ttatcaacgg acgccatgct aaaattggca 950

ccgtggtgtc tttcttttgt aacaactcct atgttcttag tggcaatgag 1000

aaaagaactt gccagcagaa tggagagtgg tcagggaaac agcccatctg 1050

cataaaagcc tgccgagaac caaagatttc agacctggtg agaaggagag 1100

ttcttccgat gcaggttcag tcaagggaga caccattaca ccagctatac 1150

tcagcggcct tcagcaagca gaaactgcag agtgccccta ccaagaagcc 1200

224

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agcccttccc tttggagatc tgcccatggg ataccaacat ctgcataccc 1250

agctccagta tgagtgcatc tcacccttct accgccgcct gggcagcagc 1300

aggaggacat gtctgaggac tgggaagtgg agtgggcggg caccatcctg 1350

catccctatc tgcgggaaaa ttgagaacat cactgctcca aagacccaag 1400

ggttgcgctg gccgtggcag gcagccatct acaggaggac cagcggggtg 1450

catgacggca gcctacacaa gggagcgtgg ttcctagtct gcagcggtgc 1500

cctggtgaat gagcgcactg tggtggtggc tgcccactgt gttactgacc 1550

tggggaaggt caccatgatc aagacagcag acctgaaagt tgttttgggg 1600

aaattctacc gggatgatga ccgggatgag aagaccatcc agagcctaca 1650

gatttctgct atcattctgc atcccaacta tgaccccatc ctgcttgatg 1700

ctgacatcgc catcctgaag ctcctagaca aggcccgtat cagcacccga 1750

gtccagccca tctgcctcgc tgccagtcgg gatctcagca cttccttcca 1800

ggagtcccac atcactgtgg ctggctggaa tgtcctggca gacgtgagga 1850

gccctggctt caagaacgac acactgcgct ctggggtggt cagtgtggtg 1900

gactcgctgc tgtgtgagga gcagcatgag gaccatggca tcccagtgag 1950

tgtcactgat aacatgttct gtgccagctg ggaacccact gccccttctg 2000

atatctgcac tgcagagaca ggaggcatcg cggctgtgtc cttcccggga 2050

cgagcatctc ctgagccacg ctggcatctg atgggactgg tcagctggag 2100

ctatgataaa acatgcagcc acaggctctc cactgccttc accaaggtgc 2150

tgccttttaa agactggatt gaaagaaata tgaaatgaac catgctcatg 2200

cactccttga gaagtgtttc tgtatatccg tctgtacgtg tgtcattgcg 2250

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gatgccaggg cttgcaagaa gtaagtttct tcaaagaaga ccatatacaa 2450

aacctctcca ctccactgac ctggtggtct tccccaactt tcagttatac 2500

gaatgccatc agcttgacca gggaagatct gggcttcatg aggccccttt 2550

tgaggctctc aagttctaga gagctgcctg tgggacagcc cagggcagca 2600

gagctgggat gtggtgcatg cctttgtgta catggccaca gtacagtctg 2650
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225

gtccttttcc ttccccatct cttgtacaca ttttaataaa ataagggttg 2700

gcttctgaac tacaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2750

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2800

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2846

<210> 231
<211> 720
<212> PRT
<213> Homo sapiens

<400> 231
Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln
 1   5   10   15

Leu Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn
                20   25   30

Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys
                35   40   45

Cys Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu
                50   55   60

Val Val Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu
                65   70   75

Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn
                80   85   90

Cys Lys Ser Cys Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp
                95   100   105

Phe Tyr Val Lys Gly Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp
                110   115   120

Tyr Gly Gly Asp Cys Met Arg Cys Gly Gln Val Leu Arg Ala Pro
                125   130   135

Lys Gly Gln Ile Leu Leu Glu Ser Tyr Pro Leu Asn Ala His Cys
                140   145   150

Glu Trp Thr Ile His Ala Lys Pro Gly Phe Val Ile Gln Leu Arg
                155   160   165

Phe Val Met Leu Ser Leu Glu Phe Asp Tyr Met Cys Gln Tyr Asp
                170   175   180

Tyr Val Glu Val Arg Asp Gly Asp Asn Arg Asp Gly Gln Ile Ile
                185   190   195

Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro Ile Gln Ser Ile
                200   205   210

Gly Ser Ser Leu His Val Leu Phe His Ser Asp Gly Ser Lys Asn
                215   220   225

226

```
Phe Asp Gly Phe His Ala Ile Tyr Glu Glu Ile Thr Ala Cys Ser
            230                 235             240

Ser Ser Pro Cys Phe His Asp Gly Thr Cys Val Leu Asp Lys Ala
            245                 250             255

Gly Ser Tyr Lys Cys Ala Cys Leu Ala Gly Tyr Thr Gly Gln Arg
            260                 265             270

Cys Glu Asn Leu Leu Glu Glu Arg Asn Cys Ser Asp Pro Gly Gly
            275                 280             285

Pro Val Asn Gly Tyr Gln Lys Ile Thr Gly Gly Pro Gly Leu Ile
            290                 295             300

Asn Gly Arg His Ala Lys Ile Gly Thr Val Val Ser Phe Phe Cys
            305                 310             315

Asn Asn Ser Tyr Val Leu Ser Gly Asn Glu Lys Arg Thr Cys Gln
            320                 325             330

Gln Asn Gly Glu Trp Ser Gly Lys Gln Pro Ile Cys Ile Lys Ala
            335                 340             345

Cys Arg Glu Pro Lys Ile Ser Asp Leu Val Arg Arg Arg Val Leu
            350                 355             360

Pro Met Gln Val Gln Ser Arg Glu Thr Pro Leu His Gln Leu Tyr
            365                 370             375

Ser Ala Ala Phe Ser Lys Gln Lys Leu Gln Ser Ala Pro Thr Lys
            380                 385             390

Lys Pro Ala Leu Pro Phe Gly Asp Leu Pro Met Gly Tyr Gln His
            395                 400             405

Leu His Thr Gln Leu Gln Tyr Glu Cys Ile Ser Pro Phe Tyr Arg
            410                 415             420

Arg Leu Gly Ser Ser Arg Arg Thr Cys Leu Arg Thr Gly Lys Trp
            425                 430             435

Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys Gly Lys Ile Glu
            440                 445             450

Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp Gln
            455                 460             465

Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu
            470                 475             480

His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn
            485                 490             495

Glu Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly
            500                 505             510

Lys Val Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly
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227

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                      515                    520                    525

      Lys Phe Tyr Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser
                      530                    535                    540

      Leu Gln Ile Ser Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile
                      545                    550                    555

      Leu Leu Asp Ala Asp Ile Ala Ile Leu Lys Leu Leu Asp Lys Ala
                      560                    565                    570

      Arg Ile Ser Thr Arg Val Gln Pro Ile Cys Leu Ala Ala Ser Arg
                      575                    580                    585

      Asp Leu Ser Thr Ser Phe Gln Glu Ser His Ile Thr Val Ala Gly
                      590                    595                    600

      Trp Asn Val Leu Ala Asp Val Arg Ser Pro Gly Phe Lys Asn Asp
                      605                    610                    615

      Thr Leu Arg Ser Gly Val Val Ser Val Val Asp Ser Leu Leu Cys
                      620                    625                    630

      Glu Glu Gln His Glu Asp His Gly Ile Pro Val Ser Val Thr Asp
                      635                    640                    645

      Asn Met Phe Cys Ala Ser Trp Glu Pro Thr Ala Pro Ser Asp Ile
                      650                    655                    660

      Cys Thr Ala Glu Thr Gly Gly Ile Ala Ala Val Ser Phe Pro Gly
                      665                    670                    675

      Arg Ala Ser Pro Glu Pro Arg Trp His Leu Met Gly Leu Val Ser
                      680                    685                    690

      Trp Ser Tyr Asp Lys Thr Cys Ser His Arg Leu Ser Thr Ala Phe
                      695                    700                    705

      Thr Lys Val Leu Pro Phe Lys Asp Trp Ile Glu Arg Asn Met Lys
                      710                    715                    720
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<210> 232
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
 aggttcgtga tggagacaac cgcg 24

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233
 tgtcaaggac gcactgccgt catg 24

<210> 234
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 234
 tggccagatc atcaagcgtg tctgtggcaa cgagcggcca gctcctatcc 50

<210> 235
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 235
 accaggcatt gtatcttcag ttgtcatcaa gttcgcaatc agattggaaa 50

 agctcaactt gaagctttct tgcctgcagt gaagcagaga gatagatatt 100

 attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttccta 150

 caaattccga ttactgttgc tgttgacttt gtgcctgaca gtggttgggt 200

 gggccaccag taactacttc gtgggtgcca ttcaagagat tcctaaagca 250

 aaggagttca tggctaattt ccataagacc ctcattttgg ggaagggaaa 300

 aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc 350

 cttctgtgtc tccttacctc agaggccaga gcaagctcat tttcaaacca 400

 gatctcactt tggaagaggt acaggcagaa aatcccaaag tgtccagagg 450

 ccggtatcgc cctcaggaat gtaaagcttt acagagggtc gccatcctcg 500

 ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg 550

 catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca 600

 ccaggctgaa ggtaaaaagt ttaatcgagc caaactcttg aatgtgggct 650

 atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat 700

 gtggacctgg tacccgagaa tgactttaac ctttacaagt gtgaggagca 750

 tcccaagcat ctggtggttg gcaggaacag cactgggtac aggttacgtt 800

 acagtggata ttttgggggt gttactgccc taagcagaga gcagtttttc 850

 aaggtgaatg gattctctaa caactactgg ggatggggag gcgaagacga 900

229

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tgacctcaga ctcagggttg agctccaaag aatgaaaatt tcccggcccc 950

tgcctgaagt gggtaaatat acaatggtct tccacactag agacaaaggc 1000

aatgaggtga acgcagaacg gatgaagctc ttacaccaag tgtcacgagt 1050

ctggagaaca gatgggttga gtagttgttc ttataaatta gtatctgtgg 1100

aacacaatcc tttatatatc aacatcacag tggatttctg gtttggtgca 1150

tgaccctgga tcttttggtg atgtttggaa gaactgattc tttgtttgca 1200

ataattttgg cctagagact tcaaatagta gcacacatta agaacctgtt 1250

acagctcatt gttgagctga atttttcctt tttgtatttt cttagcagag 1300

ctcctggtga tgtagagtat aaaacagttg taacaagaca gctttcttag 1350

tcattttgat catgagggtt aaatattgta atatggatac ttgaaggact 1400

ttatataaaa ggatgactca aaggataaaa tgaacgctat ttgaggactc 1450

tggttgaagg agatttattt aaatttgaag taatatatta tgggataaaa 1500

ggccacagga aataagactg ctgaatgtct gagagaacca gagttgttct 1550

cgtccaaggt agaaaggtac gaagatacaa tactgttatt catttatcct 1600

gtacaatcat ctgtgaagtg gtggtgtcag gtgagaaggc gtccacaaaa 1650

gaggggagaa aaggcgacga atcaggacac agtgaacttg ggaatgaaga 1700

ggtagcagga gggtggagtg tcggctgcaa aggcagcagt agctgagctg 1750

gttgcaggtg ctgatagcct tcaggggagg acctgcccag gtatgccttc 1800

cagtgatgcc caccagagaa tacattctct attagttttt aaagagtttt 1850

tgtaaaatga ttttgtacaa gtaggatatg aattagcagt ttacaagttt 1900

acatattaac taataataaa tatgtctatc aaatacctct gtagtaaaat 1950

gtgaaaaagc aaaa 1964
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<210> 236
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<221> Signal peptide
<222> 1-27
<223> Signal peptide

<220>
<221> N-glycosylation sites
<222> 4-7, 220-223, 335-338
<223> N-glycosylation sites

<220>
<221> Xylose isomerase proteins
<222> 191-201
<223> Xylose isomerase proteins

<400> 236
Met Gly Phe Asn Leu Thr Phe His Leu Ser Tyr Lys Phe Arg Leu
 1   5   10   15

Leu Leu Leu Leu Thr Leu Cys Leu Thr Val Val Gly Trp Ala Thr
                20   25   30

Ser Asn Tyr Phe Val Gly Ala Ile Gln Glu Ile Pro Lys Ala Lys
                35   40   45

Glu Phe Met Ala Asn Phe His Lys Thr Leu Ile Leu Gly Lys Gly
                50   55   60

Lys Thr Leu Thr Asn Glu Ala Ser Thr Lys Lys Val Glu Leu Asp
                65   70   75

Asn Cys Pro Ser Val Ser Pro Tyr Leu Arg Gly Gln Ser Lys Leu
                80   85   90

Ile Phe Lys Pro Asp Leu Thr Leu Glu Glu Val Gln Ala Glu Asn
                95   100   105

Pro Lys Val Ser Arg Gly Arg Tyr Arg Pro Gln Glu Cys Lys Ala
                110   115   120

Leu Gln Arg Val Ala Ile Leu Val Pro His Arg Asn Arg Glu Lys
                125   130   135

His Leu Met Tyr Leu Leu Glu His Leu His Pro Phe Leu Gln Arg
                140   145   150

Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile His Gln Ala Glu Gly
                155   160   165

Lys Lys Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Tyr Leu Glu
                170   175   180

Ala Leu Lys Glu Glu Asn Trp Asp Cys Phe Ile Phe His Asp Val
                185   190   195

Asp Leu Val Pro Glu Asn Asp Phe Asn Leu Tyr Lys Cys Glu Glu
                200   205   210

His Pro Lys His Leu Val Val Gly Arg Asn Ser Thr Gly Tyr Arg
                215   220   225

Leu Arg Tyr Ser Gly Tyr Phe Gly Gly Val Thr Ala Leu Ser Arg
                230   235   240

Glu Gln Phe Phe Lys Val Asn Gly Phe Ser Asn Asn Tyr Trp Gly
                245   250   255

Trp Gly Gly Glu Asp Asp Asp Leu Arg Leu Arg Val Glu Leu Gln

231

Arg Met Lys Ile Ser Arg Pro Leu Pro Glu Val Gly Lys Tyr Thr
                275   280   285

Met Val Phe His Thr Arg Asp Lys Gly Asn Glu Val Asn Ala Glu
                290   295   300

Arg Met Lys Leu Leu His Gln Val Ser Arg Val Trp Arg Thr Asp
                305   310   315

Gly Leu Ser Ser Cys Ser Tyr Lys Leu Val Ser Val Glu His Asn
                320   325   330

Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala
                335   340

<210> 237
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 237
 ccttacctca gaggccagag caagc 25

<210> 238
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
 gagcttcatc cgttctgcgt tcacc 25

<210> 239
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
 caggaatgta aagctttaca gagggtcgcc atcctcgttc cccacc 46

<210> 240
<211> 2567
<212> DNA
<213> Homo sapiens

<400> 240
 cgtgggccgg ggtcgcgcag cgggctgtgg gcgcgcccgg aggagcgacc 50

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gccgcagttc tcgagctcca gctgcattcc ctccgcgtcc gccccacgct 100

tctcccgctc cgggccccgc aatggcccag gcagtgtggt cgcgcctcgg 150

ccgcatcctc tggcttgcct gcctcctgcc ctgggccccg gcaggggtgg 200

ccgcaggcct gtatgaactc aatctcacca ccgatagccc tgccaccacg 250

ggagcggtgg tgaccatctc ggccagcctg gtggccaagg acaacggcag 300

cctggccctg cccgctgacg cccacctcta ccgcttccac tggatccaca 350

ccccgctggt gcttactggc aagatggaga agggtctcag ctccaccatc 400

cgtgtggtcg gccacgtgcc cggggaattc ccggtctctg tctgggtcac 450

tgccgctgac tgctggatgt gccagcctgt ggccaggggc tttgtggtcc 500

tccccatcac agagttcctc gtgggggacc ttgttgtcac ccagaacact 550

tccctaccct ggcccagctc ctatctcact aagaccgtcc tgaaagtctc 600

cttcctcctc cacgacccga gcaacttcct caagaccgcc ttgtttctct 650

acagctggga cttcggggac gggacccaga tggtgactga agactccgtg 700

gtctattata actattccat catcgggacc ttcaccgtga agctcaaagt 750

ggtggcggag tgggaagagg tggagccgga tgccacgagg gctgtgaagc 800

agaagaccgg ggacttctcc gcctcgctga agctgcagga aacccttcga 850

ggcatccaag tgttggggcc caccctaatt cagaccttcc aaaagatgac 900

cgtgaccttg aacttcctgg ggagccctcc tctgactgtg tgctggcgtc 950

tcaagcctga gtgcctcccg ctggaggaag gggagtgcca ccctgtgtcc 1000

gtggccagca cagcgtacaa cctgacccac accttcaggg accctgggga 1050

ctactgcttc agcatccggg ccgagaatat catcagcaag acacatcagt 1100

accacaagat ccaggtgtgg ccctccagaa tccagccggc tgtctttgct 1150

ttcccatgtg ctacacttat cactgtgatg ttggccttca tcatgtacat 1200

gaccctgcgg aatgccactc agcaaaagga catggtggag aacccggagc 1250

caccctctgg ggtcaggtgc tgctgccaga tgtgctgtgg gcctttcttg 1300

ctggagactc catctgagta cctggaaatt gttcgtgaga accacgggct 1350

gctcccgccc ctctataagt ctgtcaaaac ttacaccgtg tgagcactcc 1400

ccctccccac cccatctcag tgttaactga ctgctgactt ggagtttcca 1450

gcagggtggt gtgcaccact gaccaggagg ggttcatttg cgtggggctg 1500
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233

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ttggcctgga tcatccatcc atctgtacag ttcagccact gccacaagcc 1550

cctccctctc tgtcacccct gaccccagcc attcacccat ctgtacagtc 1600

cagccactga cataagcccc actcggttac cacccccttg acccctacc 1650

tttgaagagg cttcgtgcag gactttgatg cttggggtgt ccgtgttga 1700

ctcctaggtg ggcctggctg cccactgccc attcctctca tattggcaca 1750

tctgctgtcc attgggggtt ctcagtttcc tcccccagac agccctacct 1800

gtgccagaga gctagaaaga aggtcataaa gggttaaaaa tccataacta 1850

aaggttgtac acatagatgg gcacactcac agagagaagt gtgcatgtac 1900

acacaccaca cacacacaca cacacacaca cacagaaata taaacacatg 1950

cgtcacatgg gcatttcaga tgatcagctc tgtatctggt taagtcggtt 2000

gctgggatgc accctgcact agagctgaaa ggaaatttga cctccaagca 2050

gccctgacag gttctgggcc cgggccctcc ctttgtgctt tgtctctgca 2100

gttcttgcgc cctttataag gccatcctag tccctgctgg ctggcagggg 2150

cctggatggg gggcaggact aatactgagt gattgcagag tgctttataa 2200

atatcacctt attttatcga aacccatctg tgaaactttc actgaggaaa 2250

aggccttgca gcggtagaag aggttgagtc aaggccgggc gcggtggctc 2300

acgcctgtaa tcccagcact ttgggaggcc gaggcgggtg gatcacgaga 2350

tcaggagatc gagaccaccc tggctaacac ggtgaaaccc cgtctctact 2400

aaaaaaatac aaaaagttag ccgggcgtgg tggtgggtgc ctgtagtccc 2450

agctactcgg gaggctgagg caggagaatg gtgcgaaccc gggaggcgga 2500

gcttgcagtg agcccagatg gcgccactgc actccagcct gagtgacaga 2550

gcgagactct gtctcca 2567

<210> 241
<211> 423
<212> PRT
<213> Homo sapiens

<400> 241
Met Ala Gln Ala Val Trp Ser Arg Leu Gly Arg Ile Leu Trp Leu
  1               5                  10                  15

Ala Cys Leu Leu Pro Trp Ala Pro Ala Gly Val Ala Ala Gly Leu
                 20                  25                  30

Tyr Glu Leu Asn Leu Thr Thr Asp Ser Pro Ala Thr Thr Gly Ala
                 35                  40                  45
```

234

Val Val Thr Ile Ser Ala Ser Leu Val Ala Lys Asp Asn Gly Ser
          50   55   60

Leu Ala Leu Pro Ala Asp Ala His Leu Tyr Arg Phe His Trp Ile
              65   70   75

His Thr Pro Leu Val Leu Thr Gly Lys Met Glu Lys Gly Leu Ser
              80   85   90

Ser Thr Ile Arg Val Val Gly His Val Pro Gly Glu Phe Pro Val
              95   100   105

Ser Val Trp Val Thr Ala Ala Asp Cys Trp Met Cys Gln Pro Val
                  110   115   120

Ala Arg Gly Phe Val Val Leu Pro Ile Thr Glu Phe Leu Val Gly
                  125   130   135

Asp Leu Val Val Thr Gln Asn Thr Ser Leu Pro Trp Pro Ser Ser
                  140   145   150

Tyr Leu Thr Lys Thr Val Leu Lys Val Ser Phe Leu Leu His Asp
                  155   160   165

Pro Ser Asn Phe Leu Lys Thr Ala Leu Phe Leu Tyr Ser Trp Asp
                  170   175   180

Phe Gly Asp Gly Thr Gln Met Val Thr Glu Asp Ser Val Val Tyr
                  185   190   195

Tyr Asn Tyr Ser Ile Ile Gly Thr Phe Thr Val Lys Leu Lys Val
                  200   205   210

Val Ala Glu Trp Glu Glu Val Glu Pro Asp Ala Thr Arg Ala Val
                  215   220   225

Lys Gln Lys Thr Gly Asp Phe Ser Ala Ser Leu Lys Leu Gln Glu
                  230   235   240

Thr Leu Arg Gly Ile Gln Val Leu Gly Pro Thr Leu Ile Gln Thr
                  245   250   255

Phe Gln Lys Met Thr Val Thr Leu Asn Phe Leu Gly Ser Pro Pro
                  260   265   270

Leu Thr Val Cys Trp Arg Leu Lys Pro Glu Cys Leu Pro Leu Glu
                  275   280   285

Glu Gly Glu Cys His Pro Val Ser Val Ala Ser Thr Ala Tyr Asn
                  290   295   300

Leu Thr His Thr Phe Arg Asp Pro Gly Asp Tyr Cys Phe Ser Ile
                  305   310   315

Arg Ala Glu Asn Ile Ile Ser Lys Thr His Gln Tyr His Lys Ile
                  320   325   330

Gln Val Trp Pro Ser Arg Ile Gln Pro Ala Val Phe Ala Phe Pro

235

Cys Ala Thr Leu Ile Thr Val Met Leu Ala Phe Ile Met Tyr Met
            350   355   360

Thr Leu Arg Asn Ala Thr Gln Gln Lys Asp Met Val Glu Asn Pro
            365   370   375

Glu Pro Pro Ser Gly Val Arg Cys Cys Gln Met Cys Cys Gly
            380   385   390

Pro Phe Leu Leu Glu Thr Pro Ser Glu Tyr Leu Glu Ile Val Arg
            395   400   405

Glu Asn His Gly Leu Leu Pro Pro Leu Tyr Lys Ser Val Lys Thr
            410   415   420

Tyr Thr Val

<210> 242
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
 catttcctta ccctggaccc agctcc 26

<210> 243
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
 gaaaggccca cagcacatct ggcag 25

<210> 244
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 244
 ccacgacccg agcaacttcc tcaagaccga cttgtttctc tacagc 46

<210> 245
<211> 485
<212> DNA
<213> Homo sapiens

<400> 245
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga 50

gctcccagat ctgggccgct tgcctcctgc tcctcctcct cctcgccagc 100

ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct 150

gcaaccccag gacagagctg gagccagggc cagctggatg cccatgttcc 200

agaggcgaag gaggcgagac acccacttcc ccatctgcat tttctgctgc 250

ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300

acctgccctg cccccgtccc ctcccttcct tatttattcc tgctgcccca 350

gaacataggt cttggaataa aatggctggt tcttttgttt tccaaaaaaa 400

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 485

<210> 246
<211> 84
<212> PRT
<213> Homo sapiens

<400> 246
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Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu
 1               5                  10                  15

Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln
              20                  25                  30

Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala
              35                  40                  45

Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Asp
              50                  55                  60

Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg
              65                  70                  75

Ser Lys Cys Gly Met Cys Cys Lys Thr
              80
```

<210> 247
<211> 2359
<212> DNA
<213> Homo sapiens

<400> 247
ctgtcaggaa ggaccatctg aaggctgcaa tttgttctta gggaggcagg 50

tgctggcctg gcctggatct ccaccatgt tcctgttgct gccttttgat 100

agcctgattg tcaaccttct gggcatctcc ctgactgtcc tcttcaccct 150

ccttctcgtt ttcatcatag tgccagccat ttttggagtc tcctttggta 200
```

```
tccgcaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250

ttgagaatgg agcgaggagc caaggagaag aaccaccagc tttacaagcc 300

ctacaccaac ggaatcattg caaaggatcc cacttcacta gaagaagaga 350

tcaaagagat tcgtcgaagt ggtagtagta aggctctgga caacactcca 400

gagttcgagc tctctgacat tttctacttt tgccggaaag gaatggagac 450

cattatggat gatgaggtga caaagagatt ctcagcagaa gaactggagt 500

cctggaacct gctgagcaga accaattata acttccagta catcagcctt 550

cggctcacgg tcctgtgggg gttaggagtg ctgattcggt actgctttct 600

gctgccgctc aggatagcac tggctttcac agggattagc cttctggtgg 650

tgggcacaac tgtggtggga tacttgccaa atgggaggtt taaggaattc 700

atgagtaaac atgttcactt aatgtgttac cggatctgcg tgcgagcgct 750

gacagccatc atcacctacc atgacaggga aaacagacca agaaatggtg 800

gcatctgtgt ggccaatcat acctcaccga tcgatgtgat catcttggcc 850

agcgatggct attatgccat ggtgggtcaa gtgcacgggg gactcatggg 900

tgtgattcag agagccatgg tgaaggcctg cccacacgtc tggtttgagc 950

gctcggaagt gaaggatcgc cacctggtgg ctaagagact gactgaacat 1000

gtgcaagata aaagcaagct gcctatcctc atcttcccag aaggaacctg 1050

catcaataat acatcggtga tgatgttcaa aaagggaagt tttgaaattg 1100

gagccacagt ttaccctgtt gctatcaagt atgaccctca atttggcgat 1150

gccttctgga acagcagcaa atacgggatg gtgacgtacc tgctgcgaat 1200

gatgaccagc tgggccattg tctgcagcgt gtggtacctg cctcccatga 1250

ctagagaggc agatgaagat gctgtccagt ttgcgaatag ggtgaaatct 1300

gccattgcca ggcagggagg acttgtggac ctgctgtggg atgggggcct 1350

gaagagggag aaggtgaagg acacgttcaa ggaggagcag cagaagctgt 1400

acagcaagat gatcgtgggg aaccacaagg acaggagccg ctcctgagcc 1450

tgcctccagc tggctggggc caccgtgcgg ggtgccaacg ggctcagagc 1500

tggagttgcc gccgccgccc ccactgctgt gtcctttcca gactccaggg 1550

ctccccgggc tgctctggat cccaggactc cggctttcgc cgagccgcag 1600

cgggatccct gtgcacccgg cgcagcctac ccttggtggt ctaaacggat 1650
```

238

```
gctgctgggt gttgcgaccc aggacgagat gccttgtttc ttttacaata 1700

agtcgttgga ggaatgccat taaagtgaac tccccacctt tgcacgctgt 1750

gcgggctgag tggttggggga gatgtggcca tggtcttgtg ctagagatgg 1800

cggtacaaga gtctgttatg caagcccgtg tgccagggat gtgctggggg 1850

cggccacccg ctctccagga aaggcacagc tgaggcactg tggctggctt 1900

cggcctcaac atcgccccca gccttggagc tctgcagaca tgataggaag 1950

gaaactgtca tctgcagggg ctttcagcaa aatgaagggt tagattttta 2000

tgctgctgct gatggggtta ctaaagggag gggaagaggc caggtgggcc 2050

gctgactggg ccatggggag aacgtgtgtt cgtactccag gctaaccctg 2100

aactccccat gtgatgcgcg ctttgttgaa tgtgtgtctc ggtttcccca 2150

tctgtaatat gagtcggggg gaatggtggt gattcctacc tcacagggct 2200

gttgtgggga ttaaagtgct gcgggtgagt gaaggacaca tcacgttcag 2250

tgtttcaagt acaggcccac aaaacggggc acggcaggcc tgagctcaga 2300

gctgctgcac tgggctttgg atttgttctt gtgagtaaat aaaactggct 2350

ggtgaatga 2359

<210> 248
<211> 456
<212> PRT
<213> Homo sapiens

<400> 248
Met Phe Leu Leu Leu Pro Phe Asp Ser Leu Ile Val Asn Leu Leu
1               5                   10                  15

Gly Ile Ser Leu Thr Val Leu Phe Thr Leu Leu Leu Val Phe Ile
                20                  25                  30

Ile Val Pro Ala Ile Phe Gly Val Ser Phe Gly Ile Arg Lys Leu
                35                  40                  45

Tyr Met Lys Ser Leu Leu Lys Ile Phe Ala Trp Ala Thr Leu Arg
                50                  55                  60

Met Glu Arg Gly Ala Lys Glu Lys Asn His Gln Leu Tyr Lys Pro
                65                  70                  75

Tyr Thr Asn Gly Ile Ile Ala Lys Asp Pro Thr Ser Leu Glu Glu
                80                  85                  90

Glu Ile Lys Glu Ile Arg Arg Ser Gly Ser Ser Lys Ala Leu Asp
                95                  100                 105

Asn Thr Pro Glu Phe Glu Leu Ser Asp Ile Phe Tyr Phe Cys Arg
```

239

```
                110                    115                   120
Lys Gly Met Glu Thr Ile Met Asp Asp Glu Val Thr Lys Arg Phe
                125                   130                   135
Ser Ala Glu Glu Leu Glu Ser Trp Asn Leu Leu Ser Arg Thr Asn
                140                   145                   150
Tyr Asn Phe Gln Tyr Ile Ser Leu Arg Leu Thr Val Leu Trp Gly
                155                   160                   165
Leu Gly Val Leu Ile Arg Tyr Cys Phe Leu Leu Pro Leu Arg Ile
                170                   175                   180
Ala Leu Ala Phe Thr Gly Ile Ser Leu Leu Val Val Gly Thr Thr
                185                   190                   195
Val Val Gly Tyr Leu Pro Asn Gly Arg Phe Lys Glu Phe Met Ser
                200                   205                   210
Lys His Val His Leu Met Cys Tyr Arg Ile Cys Val Arg Ala Leu
                215                   220                   225
Thr Ala Ile Ile Thr Tyr His Asp Arg Glu Asn Arg Pro Arg Asn
                230                   235                   240
Gly Gly Ile Cys Val Ala Asn His Thr Ser Pro Ile Asp Val Ile
                245                   250                   255
Ile Leu Ala Ser Asp Gly Tyr Tyr Ala Met Val Gly Gln Val His
                260                   265                   270
Gly Gly Leu Met Gly Val Ile Gln Arg Ala Met Val Lys Ala Cys
                275                   280                   285
Pro His Val Trp Phe Glu Arg Ser Glu Val Lys Asp Arg His Leu
                290                   295                   300
Val Ala Lys Arg Leu Thr Glu His Val Gln Asp Lys Ser Lys Leu
                305                   310                   315
Pro Ile Leu Ile Phe Pro Glu Gly Thr Cys Ile Asn Asn Thr Ser
                320                   325                   330
Val Met Met Phe Lys Lys Gly Ser Phe Glu Ile Gly Ala Thr Val
                335                   340                   345
Tyr Pro Val Ala Ile Lys Tyr Asp Pro Gln Phe Gly Asp Ala Phe
                350                   355                   360
Trp Asn Ser Ser Lys Tyr Gly Met Val Thr Tyr Leu Leu Arg Met
                365                   370                   375
Met Thr Ser Trp Ala Ile Val Cys Ser Val Trp Tyr Leu Pro Pro
                380                   385                   390
Met Thr Arg Glu Ala Asp Glu Asp Ala Val Gln Phe Ala Asn Arg
                395                   400                   405
```

240

Val Lys Ser Ala Ile Ala Arg Gln Gly Gly Leu Val Asp Leu Leu
               410   415   420

Trp Asp Gly Gly Leu Lys Arg Glu Lys Val Lys Asp Thr Phe Lys
               425   430   435

Glu Glu Gln Gln Lys Leu Tyr Ser Lys Met Ile Val Gly Asn His
               440   445   450

Lys Asp Arg Ser Arg Ser
               455

<210> 249
<211> 1103
<212> DNA
<213> Homo sapiens

<400> 249
gcccctcgaa accaggactc cagcacctct ggtcccgccc tcacccggac 50

ccctggccct cacgtctcct ccagggatgg cgctggcggc tttgatgatc 100

gccctcggca gcctcggcct ccacacctgg caggcccagg ctgttcccac 150

catcctgccc ctgggcctgg ctccagacac ctttgacgat acctatgtgg 200

gttgtgcaga ggagatggag gagaaggcag ccccctgct aaaggaggaa 250

atggcccacc atgccctgct gcgggaatcc tgggaggcag cccaggagac 300

ctgggaggac aagcgtcgag ggcttacctt gccccctggc ttcaaagccc 350

agaatggaat agccattatg gtctacacca actcatcgaa caccttgtac 400

tgggagttga atcaggccgt gcggacgggc ggaggctccc gggagctcta 450

catgaggcac tttcccttca aggccctgca tttctacctg atccgggccc 500

tgcagctgct gcgaggcagt gggggctgca gcaggggacc tggggaggtg 550

gtgttccgag gtgtgggcag ccttcgcttt gaacccaaga ggctggggga 600

ctctgtccgc ttgggccagt ttgcctccag ctccctggat aaggcagtgg 650

cccacagatt tggggagaag aggcggggct gtgtgtctgc gccagggggtg 700

cagctagggt cacaatctga ggggggcctcc tctctgcccc cctggaagac 750

tctgctcttg gcccctggag agttccagct ctcagggggtt gggccctgaa 800

agtccaacat ctgccactta ggagccctgg aacgggtga ccttcatatg 850

acgaagaggc acctccagca gccttgagaa gcaagaacat ggttccggac 900

ccagccctag cagccttctc cccaaccagg atgttggcct ggggaggcca 950

cagcagggct gagggaactc tgctatgtga tggggacttc ctgggacaag 1000

caaggaaagt actgaggcag ccacttgatt gaacggtgtt gcaatgtgga 1050

gacatggagt tttattgagg tagctacgtg attaaatggt attgcagtgt 1100

gga 1103

<210> 250
<211> 240
<212> PRT
<213> Homo sapiens

<400> 250
Met Ala Leu Ala Ala Leu Met Ile Ala Leu Gly Ser Leu Gly Leu
1   5   10   15

His Thr Trp Gln Ala Gln Ala Val Pro Thr Ile Leu Pro Leu Gly
                20   25   30

Leu Ala Pro Asp Thr Phe Asp Asp Thr Tyr Val Gly Cys Ala Glu
                35   40   45

Glu Met Glu Glu Lys Ala Ala Pro Leu Leu Lys Glu Glu Met Ala
                50   55   60

His His Ala Leu Leu Arg Glu Ser Trp Glu Ala Ala Gln Glu Thr
                65   70   75

Trp Glu Asp Lys Arg Arg Gly Leu Thr Leu Pro Pro Gly Phe Lys
                80   85   90

Ala Gln Asn Gly Ile Ala Ile Met Val Tyr Thr Asn Ser Ser Asn
                95   100   105

Thr Leu Tyr Trp Glu Leu Asn Gln Ala Val Arg Thr Gly Gly Gly
                110   115   120

Ser Arg Glu Leu Tyr Met Arg His Phe Pro Phe Lys Ala Leu His
                125   130   135

Phe Tyr Leu Ile Arg Ala Leu Gln Leu Leu Arg Gly Ser Gly Gly
                140   145   150

Cys Ser Arg Gly Pro Gly Glu Val Val Phe Arg Gly Val Gly Ser
                155   160   165

Leu Arg Phe Glu Pro Lys Arg Leu Gly Asp Ser Val Arg Leu Gly
                170   175   180

Gln Phe Ala Ser Ser Ser Leu Asp Lys Ala Val Ala His Arg Phe
                185   190   195

Gly Glu Lys Arg Arg Gly Cys Val Ser Ala Pro Gly Val Gln Leu
                200   205   210

Gly Ser Gln Ser Glu Gly Ala Ser Ser Leu Pro Pro Trp Lys Thr
                215   220   225

Leu Leu Leu Ala Pro Gly Glu Phe Gln Leu Ser Gly Val Gly Pro

242

<210> 251
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
 ccaccacctg gaggtcctgc agttgggcag gaactccatc cggcagattg 50

<210> 252
<211> 1076
<212> DNA
<213> Homo sapiens

<400> 252
 gtggcttcat ttcagtggct gacttccaga gagcaatatg gctggttccc 50

 caacatgcct caccctcatc tatatccttt ggcagctcac agggtcagca 100

 gcctctggac ccgtgaaaga gctggtcggt tccgttggtg gggccgtgac 150

 tttcccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200

 tcaacacaac ccctcttgtc accatacagc cagaaggggg cactatcata 250

 gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta 300

 ctccctgaag ctcagcaaac tgaagaagaa tgactcaggg atctactatg 350

 tggggatata cagctcatca ctccagcagc cctccaccca ggagtacgtg 400

 ctgcatgtct acgagcacct gtcaaagcct aaagtcacca tgggtctgca 450

 gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcatggaac 500

 atgggaaga ggatgtgatt tatacctgga aggccctggg gcaagcagcc 550

 aatgagtccc ataatgggtc catcctcccc atctcctgga gatggggaga 600

 aagtgatatg accttcatct gcgttgccag gaaccctgtc agcagaaact 650

 tctcaagccc catccttgcc aggaagctct gtgaaggtgc tgctgatgac 700

 ccagattcct ccatggtcct cctgtgtctc ctgttggtgc ccctcctgct 750

 cagtctcttt gtactggggc tatttctttg gtttctgaag agagagagac 800

 aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact 850

 cctaacatat gcccccattc tggagagaac acagagtacg acacaatccc 900

 tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact 950

 ccactgtgga aataccgaaa aagatggaaa atccccactc actgctcacg 1000

243

atgccagaca caccaaggct atttgcctat gagaatgtta tctagacagc 1050

agtgcactcc cctaagtctc tgctca 1076

<210> 253
<211> 335
<212> PRT
<213> Homo sapiens

<400> 253

```
Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp
 1               5                  10                  15

Gln Leu Thr Gly Ser Ala Ala Ser Gly Pro Val Lys Glu Leu Val
                20                  25                  30

Gly Ser Val Gly Gly Ala Val Thr Phe Pro Leu Lys Ser Lys Val
                35                  40                  45

Lys Gln Val Asp Ser Ile Val Trp Thr Phe Asn Thr Thr Pro Leu
                50                  55                  60

Val Thr Ile Gln Pro Glu Gly Gly Thr Ile Ile Val Thr Gln Asn
                65                  70                  75

Arg Asn Arg Glu Arg Val Asp Phe Pro Asp Gly Gly Tyr Ser Leu
                80                  85                  90

Lys Leu Ser Lys Leu Lys Lys Asn Asp Ser Gly Ile Tyr Tyr Val
                95                  100                 105

Gly Ile Tyr Ser Ser Ser Leu Gln Gln Pro Ser Thr Gln Glu Tyr
                110                 115                 120

Val Leu His Val Tyr Glu His Leu Ser Lys Pro Lys Val Thr Met
                125                 130                 135

Gly Leu Gln Ser Asn Lys Asn Gly Thr Cys Val Thr Asn Leu Thr
                140                 145                 150

Cys Cys Met Glu His Gly Glu Glu Asp Val Ile Tyr Thr Trp Lys
                155                 160                 165

Ala Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu
                170                 175                 180

Pro Ile Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys
                185                 190                 195

Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser Pro Ile Leu
                200                 205                 210

Ala Arg Lys Leu Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser Ser
                215                 220                 225

Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu
                230                 235                 240
```

244

Phe Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln
            245   250   255

Glu Glu Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu
            260   265   270

Thr Pro Asn Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp
            275   280   285

Thr Ile Pro His Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala
            290   295   300

Asn Thr Val Tyr Ser Thr Val Glu Ile Pro Lys Lys Met Glu Asn
            305   310   315

Pro His Ser Leu Leu Thr Met Pro Asp Thr Pro Arg Leu Phe Ala
            320   325   330

Tyr Glu Asn Val Ile
            335

<210> 254
<211> 1053
<212> DNA
<213> Homo sapiens

<400> 254
ctggttcccc aacatgcctc accctcatct atatcctttg gcagctcaca 50

gggtcagcag cctctggacc cgtgaaagag ctggtcggtt ccgttggtgg 100

ggccgtgact ttccccctga agtccaaagt aaagcaagtt gactctattg 150

tctggacctt caacacaacc cctcttgtca ccatacagcc agaagggggc 200

actatcatag tgacccaaaa tcgtaatagg gagagagtag acttcccaga 250

tggaggctac tccctgaagc tcagcaaact gaagaagaat gactcaggga 300

tctactatgt ggggatatac agctcatcac tccagcagcc ctccacccag 350

gagtacgtgc tgcatgtcta cgagcacctg tcaaagccta aagtcaccat 400

gggtctgcag agcaataaga atggcacctg tgtgaccaat ctgacatgct 450

gcatggaaca tggggaagag gatgtgattt atacctggaa ggccctgggg 500

caagcagcca atgagtccca taatgggtcc atcctcccca tctcctggag 550

atggggagaa agtgatatga ccttcatctg cgttgccagg aaccctgtca 600

gcagaaactt ctcaagcccc atccttgcca ggaagctctg tgaaggtgct 650

gctgatgacc cagattcctc catggtcctc ctgtgtctcc tgttggtgcc 700

cctcctgctc agtctctttg tactggggct atttctttgg tttctgaaga 750

gagagagaca agaagagtac attgaagaga agaagagagt ggacatttgt 800

cggggaaactc ctaacatatg cccccattct ggagagaaca cagagtacga 850

cacaatccct cacactaata gaacaatcct aaaggaagat ccagcaaata 900

cggtttactc cactgtggaa ataccgaaaa agatggaaaa tccccactca 950

ctgctcacga tgccagacac accaaggcta tttgcctatg agaatgttat 1000

ctagacagca gtgcactccc ctaagtctct gctcaaaaaa aaaaaaaaaa 1050

aaa 1053

<210> 255
<211> 860
<212> DNA
<213> Homo sapiens

<400> 255
gaaagacgtg gtcctgacag acagacaatc ctattcccta ccaaaatgaa 50

gatgctgctg ctgctgtgtt tgggactgac cctagtctgt gtccatgcag 100

aagaagctag ttctacggga aggaacttta atgtagaaaa gattaatggg 150

gaatggcata ctattatcct ggcctctgac aaaagagaaa agatagaaga 200

acatggcaac tttagacttt ttctggagca aatccatgtc ttggagaatt 250

ccttagttct taaagtccat actgtaagag atgaagagtg ctccgaatta 300

tctatggttg ctgacaaaac agaaaaggct ggtgaatatt ctgtgacgta 350

tgatggattc aatacattta ctatacctaa gacagactat gataactttc 400

ttatggctca cctcattaac gaaaaggatg gggaaacctt ccagctgatg 450

gggctctatg gccgagaacc agatttgagt tcagacatca aggaaaggtt 500

tgcacaacta tgtgaggagc atggaatcct tagagaaaat atcattgacc 550

tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggcctga 600

gcctccagtg ttgagtggac acttctcacc aggactccac catcatccct 650

tcctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700

ctgtctcact gagaagtcca attccagtct atcaacatgt tacctaggat 750

acctcatcaa gaatcaaaga cttctttaaa tttctctttg atacacccctt 800

gacaatttt catgaaatta ttcctcttcc tgttcaataa atgattaccc 850

ttgcacttaa 860

<210> 256
<211> 180
<212> PRT
<213> Homo sapiens

246

<400> 256
Met Lys Met Leu Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys
 1   5   10   15

Val His Ala Glu Glu Ala Ser Ser Thr Gly Arg Asn Phe Asn Val
                20   25   30

Glu Lys Ile Asn Gly Glu Trp His Thr Ile Ile Leu Ala Ser Asp
                35   40   45

Lys Arg Glu Lys Ile Glu Glu His Gly Asn Phe Arg Leu Phe Leu
                50   55   60

Glu Gln Ile His Val Leu Glu Asn Ser Leu Val Leu Lys Val His
                65   70   75

Thr Val Arg Asp Glu Glu Cys Ser Glu Leu Ser Met Val Ala Asp
                80   85   90

Lys Thr Glu Lys Ala Gly Glu Tyr Ser Val Thr Tyr Asp Gly Phe
                95   100   105

Asn Thr Phe Thr Ile Pro Lys Thr Asp Tyr Asp Asn Phe Leu Met
                110   115   120

Ala His Leu Ile Asn Glu Lys Asp Gly Glu Thr Phe Gln Leu Met
                125   130   135

Gly Leu Tyr Gly Arg Glu Pro Asp Leu Ser Ser Asp Ile Lys Glu
                140   145   150

Arg Phe Ala Gln Leu Cys Glu Glu His Gly Ile Leu Arg Glu Asn
                155   160   165

Ile Ile Asp Leu Ser Asn Ala Asn Arg Cys Leu Gln Ala Arg Glu
                170   175   180

<210> 257
<211> 766
<212> DNA
<213> Homo sapiens

<400> 257
ggctcgagcg tttctgagcc aggggtgacc atgacctgct gcgaaggatg 50

gacatcctgc aatggattca gcctgctggt tctactgctg ttaggagtag 100

ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaattt 150

tctcaaaacc ccatctcttg ctttgagtgg tggttcccag gaattatagg 200

agcaggtctg atggccattc agcaacaac aatgtccttg acagcaagaa 250

aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300

agtgtgatca cagtcattgg tgctctgtat tgcatgctga tatccatcca 350

ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg 400

247

ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450

ttcaacttgc agtggttttt caatgactct tgtgcacctc ctactggttt 500

caataaaccc accagtaacg acaccatggc gagtggctgg agagcatcta 550

gtttccactt cgattctgaa gaaaacaaac ataggcttat ccacttctca 600

gtattttag gtctattgct tgttggaatt ctggaggtcc tgtttgggct 650

cagtcagata gtcatcggtt tccttggctg tctgtgtgga gtctctaagc 700

gaagaagtca aattgtgtag tttaatggga ataaaatgta agtatcagta 750

gtttgaaaaa aaaaaa 766

<210> 258
<211> 229
<212> PRT
<213> Homo sapiens

<400> 258
Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu
  1   5   10   15

Leu Val Leu Leu Leu Leu Gly Val Val Leu Asn Ala Ile Pro Leu
               20   25   30

Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile
               35   40   45

Ser Cys Phe Glu Trp Trp Phe Pro Gly Ile Ile Gly Ala Gly Leu
               50   55   60

Met Ala Ile Pro Ala Thr Thr Met Ser Leu Thr Ala Arg Lys Arg
               65   70   75

Ala Cys Cys Asn Asn Arg Thr Gly Met Phe Leu Ser Ser Phe Phe
               80   85   90

Ser Val Ile Thr Val Ile Gly Ala Leu Tyr Cys Met Leu Ile Ser
               95   100   105

Ile Gln Ala Leu Leu Lys Gly Pro Leu Met Cys Asn Ser Pro Ser
               110   115   120

Asn Ser Asn Ala Asn Cys Glu Phe Ser Leu Lys Asn Ile Ser Asp
               125   130   135

Ile His Pro Glu Ser Phe Asn Leu Gln Trp Phe Phe Asn Asp Ser
               140   145   150

Cys Ala Pro Pro Thr Gly Phe Asn Lys Pro Thr Ser Asn Asp Thr
               155   160   165

Met Ala Ser Gly Trp Arg Ala Ser Ser Phe His Phe Asp Ser Glu
               170   175   180

248

```
Glu Asn Lys His Arg Leu Ile His Phe Ser Val Phe Leu Gly Leu
                185                 190                 195

Leu Leu Val Gly Ile Leu Glu Val Leu Phe Gly Leu Ser Gln Ile
                200                 205                 210

Val Ile Gly Phe Leu Gly Cys Leu Cys Gly Val Ser Lys Arg Arg
                215                 220                 225

Ser Gln Ile Val


<210> 259
<211> 434
<212> DNA
<213> Homo sapiens

<400> 259
 gtcgaatcca aatcactcat tgtgaaagct gagctcacag ccgaataagc 50

 caccatgagg ctgtcagtgt gtctcctgat ggtctcgctg gcccttttgct 100

 gctaccaggc ccatgctctt gtctgcccag ctgttgcttc tgagatcaca 150

 gtcttcttat tcttaagtga cgctgcggta aacctccaag ttgccaaact 200

 taatccacct ccagaagctc ttgcagccaa gttggaagtg aagcactgca 250

 ccgatcagat atctttttaag aaacgactct cattgaaaaa gtcctggtgg 300

 aaatagtgaa aaaatgtggt gtgtgacatg taaaaatgct caacctggtt 350

 tccaaagtct ttcaacgaca ccctgatctt cactaaaaat tgtaaaggtt 400

 tcaacacgtt gctttaataa atcacttgcc ctgc 434

<210> 260
<211> 83
<212> PRT
<213> Homo sapiens

<400> 260
 Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys
   1               5                  10                  15

 Cys Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu
                 20                  25                  30

 Ile Thr Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln
                 35                  40                  45

 Val Ala Lys Leu Asn Pro Pro Glu Ala Leu Ala Ala Lys Leu
                 50                  55                  60

 Glu Val Lys His Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu
                 65                  70                  75

 Ser Leu Lys Lys Ser Trp Trp Lys
```

<210> 261
<211> 636
<212> DNA
<213> Homo sapiens

<400> 261
atccgttctc tgcgctgcca gctcaggtga gccctcgcca aggtgacctc 50

gcaggacact ggtgaaggag cagtgaggaa cctgcagagt cacacagttg 100

ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150

cgccccagtg cctctccccc tgcagccctg cccctcgaac tgtgacatgg 200

agagagtgac cctggccctt ctcctactgg caggcctgac tgccttggaa 250

gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa 300

aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg 350

ggatcgcggc agttctgagt ggcaaatgca aatacaagag cagccagaag 400

cagcacagtc ctgtacctga aaggccatc ccactcatca ctccaggctc 450

tgccactact tgctgagcac aggactggcc tccagggatg gcctgaagcc 500

taacactggc ccccagcacc tcctcccctg ggaggcctta tcctcaagga 550

aggacttctc tccaagggca ggctgttagg ccccttctg atcaggaggc 600

ttctttatga attaaactcg ccccaccacc ccctca 636

<210> 262
<211> 89
<212> PRT
<213> Homo sapiens

<400> 262
Met Glu Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr
1   5   10   15

Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe
                20   25   30

Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly
                35   40   45

Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys
                50   55   60

Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu
                65   70   75

Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys
                80   85

<210> 263
<211> 1676
<212> DNA
<213> Homo sapiens

<400> 263
ggagaagagg ttgtgtggga caagctgctc ccgacagaag gatgtcgctg 50

ctgagcctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct 100

actcctgctg ctggttgtgg gctcctggct actcgcccgc atcctggctt 150

ggacctatgc cttctataac aactgccgcc ggctccagtg tttcccacag 200

cccccaaaac ggaactggtt ttggggtcac ctgggcctga tcactcctac 250

agaggagggc ttgaaggact cgacccagat gtcggccacc tattcccagg 300

gctttacggt atggctgggt cccatcatcc ccttcatcgt tttatgccac 350

cctgacacca tccggtctat caccaatgcc tcagctgcca ttgcacccaa 400

ggataatctc ttcatcaggt tcctgaagcc ctggctggga gaagggatac 450

tgctgagtgg cggtgacaag tggagccgcc accgtcggat gctgacgccc 500

gccttccatt tcaacatcct gaagtcctat ataacgatct tcaacaagag 550

tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca 600

gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta 650

cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga 700

atatattgcc accatcttgg agctcagtgc ccttgtagag aaaagaagcc 750

agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg 800

cggcgcttcc acagggcctg ccgcctggtg catgacttca cagacgctgt 850

catccgggag cggcgtcgca ccctccccac tcagggtatt gatgattttt 900

tcaaagacaa agccaagtcc aagactttgg atttcattga tgtgcttctg 950

ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc 1000

agaggctgac accttcatgt ttgaggccat gacaccacg gccagtggcc 1050

tctcctgggt cctgtacaac cttgcgaggc acccagaata ccaggagcgc 1100

tgccgacagg aggtgcaaga gcttctgaag accgcgatc ctaaagagat 1150

tgaatgggac gacctggccc agctgccctt cctgaccatg tgcgtgaagg 1200

agagcctgag gttacatccc ccagctccct tcatctcccg atgctgcacc 1250

caggacattg ttctcccaga tggccgagtc atccccaaag gcattacctg 1300

cctcatcgat attatagggg tccatcacaa cccaactgtg tggccggatc 1350

ctgaggtcta cgacccttc cgctttgacc cagagaacag caaggggagg 1400

tcacctctgg cttttattcc tttctccgca gggcccagga actgcatcgg 1450

gcaggcgttc gccatggcgg agatgaaagt ggtcctggcg ttgatgctgc 1500

tgcacttccg gttcctgcca gaccacactg agccccgcag gaagctggaa 1550

ttgatcatgc gcgccgaggg cgggctttgg ctgcgggtgg agcccctgaa 1600

tgtaggcttg cagtgacttt ctgacccatc cacctgtttt tttgcagatt 1650

gtcatgaata aaacggtgct gtcaaa 1676

<210> 264
<211> 524
<212> PRT
<213> Homo sapiens

<400> 264
Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala
1   5   10   15

Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu
                20   25   30

Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys
                35   40   45

Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe
                50   55   60

Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys
                65   70   75

Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val
                80   85   90

Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp
                95   100   105

Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys
                110   115   120

Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly
                125   130   135

Ile Leu Leu Ser Gly Gly Asp Lys Trp Ser Arg His Arg Arg Met
                140   145   150

Leu Thr Pro Ala Phe His Phe Asn Ile Leu Lys Ser Tyr Ile Thr
                155   160   165

Ile Phe Asn Lys Ser Ala Asn Ile Met Leu Asp Lys Trp Gln His
                170   175   180

252

```
Leu Ala Ser Glu Gly Ser Ser Arg Leu Asp Met Phe Glu His Ile
                185                 190                 195

Ser Leu Met Thr Leu Asp Ser Leu Gln Lys Cys Ile Phe Ser Phe
                200                 205                 210

Asp Ser His Cys Gln Glu Arg Pro Ser Glu Tyr Ile Ala Thr Ile
                215                 220                 225

Leu Glu Leu Ser Ala Leu Val Glu Lys Arg Ser Gln His Ile Leu
                230                 235                 240

Gln His Met Asp Phe Leu Tyr Tyr Leu Ser His Asp Gly Arg Arg
                245                 250                 255

Phe His Arg Ala Cys Arg Leu Val His Asp Phe Thr Asp Ala Val
                260                 265                 270

Ile Arg Glu Arg Arg Arg Thr Leu Pro Thr Gln Gly Ile Asp Asp
                275                 280                 285

Phe Phe Lys Asp Lys Ala Lys Ser Lys Thr Leu Asp Phe Ile Asp
                290                 295                 300

Val Leu Leu Leu Ser Lys Asp Glu Asp Gly Lys Ala Leu Ser Asp
                305                 310                 315

Glu Asp Ile Arg Ala Glu Ala Asp Thr Phe Met Phe Gly Gly His
                320                 325                 330

Asp Thr Thr Ala Ser Gly Leu Ser Trp Val Leu Tyr Asn Leu Ala
                335                 340                 345

Arg His Pro Glu Tyr Gln Glu Arg Cys Arg Gln Glu Val Gln Glu
                350                 355                 360

Leu Leu Lys Asp Arg Asp Pro Lys Glu Ile Glu Trp Asp Asp Leu
                365                 370                 375

Ala Gln Leu Pro Phe Leu Thr Met Cys Val Lys Glu Ser Leu Arg
                380                 385                 390

Leu His Pro Pro Ala Pro Phe Ile Ser Arg Cys Cys Thr Gln Asp
                395                 400                 405

Ile Val Leu Pro Asp Gly Arg Val Ile Pro Lys Gly Ile Thr Cys
                410                 415                 420

Leu Ile Asp Ile Ile Gly Val His His Asn Pro Thr Val Trp Pro
                425                 430                 435

Asp Pro Glu Val Tyr Asp Pro Phe Arg Phe Asp Pro Glu Asn Ser
                440                 445                 450

Lys Gly Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly Pro
                455                 460                 465

Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val
```

253

Val Leu Ala Leu Met Leu Leu His Phe Arg Phe Leu Pro Asp His
                485   490   495

Thr Glu Pro Arg Arg Lys Leu Glu Leu Ile Met Arg Ala Glu Gly
                500   505   510

Gly Leu Trp Leu Arg Val Glu Pro Leu Asn Val Gly Leu Gln
                515   520

<210> 265
<211> 584
<212> DNA
<213> Homo sapiens

<400> 265
caacagaagc caagaaggaa gccgtctatc ttgtggcgat catgtataag 50

ctggcctcct gctgtttgct tttcacagga ttcttaaatc ctctcttatc 100

tcttcctctc cttgactcca gggaaatatc ctttcaactc tcagcacctc 150

atgaagacgc gcgcttaact ccggaggagc tagaaagagc ttcccttcta 200

cagatattgc cagagatgct gggtgcagaa agaggggata ttctcaggaa 250

agcagactca agtaccaaca ttttaaccc aagaggaaat ttgagaaagt 300

ttcaggattt ctctggacaa gatcctaaca ttttactgag tcatcttttg 350

gccagaatct ggaaaccata caagaaacgt gagactcctg attgcttctg 400

gaaatactgt gtctgaagtg aaataagcat ctgttagtca gctcagaaac 450

acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagtg 500

tggagaaaaa ctaggcaaac tacaccctgt tcattgttac ctggaaaata 550

aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266
<211> 124
<212> PRT
<213> Homo sapiens

<400> 266
Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu
  1   5   10   15

Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser
                20   25   30

Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu
                35   40   45

Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu
                50   55   60

Gly Ala Glu Arg Gly Asp Ile Leu Arg Lys Ala Asp Ser Ser Thr
                65   70   75

Asn Ile Phe Asn Pro Arg Gly Asn Leu Arg Lys Phe Gln Asp Phe
                80   85   90

Ser Gly Gln Asp Pro Asn Ile Leu Leu Ser His Leu Leu Ala Arg
                95   100   105

Ile Trp Lys Pro Tyr Lys Lys Arg Glu Thr Pro Asp Cys Phe Trp
               110   115   120

Lys Tyr Cys Val

<210> 267
<211> 654
<212> DNA
<213> Homo sapiens

<400> 267
  gaacattttt agttcccaag gaatgtacat cagccccacg gaagctaggc 50

  cacctctggg atggggttgc tggtttaaaa caaacgccag tcatcctata 100

  taaggacctg acagccacca ggcaccacct ccgccaggaa ctgcaggccc 150

  acctgtctgc aacccagctg aggccatgcc ctccccaggg accgtctgca 200

  gcctcctgct cctcggcatg ctctggctgg acttggccat ggcaggctcc 250

  agcttcctga gccctgaaca ccagagagtc cagcagagaa aggagtcgaa 300

  gaagccacca gccaagctgc agccccgagc tctagcaggc tggctccgcc 350

  cggaagatgg aggtcaagca gaaggggcag aggatgaact ggaagtccgg 400

  ttcaacgccc cctttgatgt tggaatcaag ctgtcagggg ttcagtacca 450

  gcagcacagc caggccctgg ggaagtttct tcaggacatc ctctgggaag 500

  aggccaaaga ggccccagcc gacaagtgat cgcccacaag ccttactcac 550

  ctctctctaa gtttagaagc gctcatctgg cttttcgctt gcttctgcag 600

  caactcccac gactgttgta caagctcagg aggcgaataa atgttcaaac 650

  tgta 654

<210> 268
<211> 117
<212> PRT
<213> Homo sapiens

<400> 268
  Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met
   1   5   10   15

255

Leu Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro
                  20   25   30

Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro
                  35   40   45

Ala Lys Leu Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu
                  50   55   60

Asp Gly Gly Gln Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg
                  65   70   75

Phe Asn Ala Pro Phe Asp Val Gly Ile Lys Leu Ser Gly Val Gln
                  80   85   90

Tyr Gln Gln His Ser Gln Ala Leu Gly Lys Phe Leu Gln Asp Ile
                  95   100   105

Leu Trp Glu Glu Ala Lys Glu Ala Pro Ala Asp Lys
                  110   115

<210> 269
<211> 1332
<212> DNA
<213> Homo sapiens

<400> 269
cggccacagc tggcatgctc tgcctgatcg ccatcctgct gtatgtcctc 50

gtccagtacc tcgtgaaccc cggggtgctc cgcacggacc ccagatgtca 100

agaatatgaa cacgtggctg ctgttcctcc ccctgttccc ggtgcaggtg 150

cagaccctga tagtcgtgat catcgggatg ctcgtgctcc tgctggactt 200

tcttggcttg gtgcacctgg gccagctgct catcttccac atctacctga 250

gtatgtcccc caccctaagc ccccgatccc cccaaggctg ggtggtcaga 300

gctgctcatc ttacacctct acttgagtat gtccctaacc ctgagccccc 350

cacgcctggg gccagagtct ttgtcccccg tgtgcgcatg tgttcagggt 400

cagcctctcc cagaagtgag atcatggaca aaaagggcaa atcacaggaa 450

gaaattaaat ccatgaggac ccagcaggcc cagcaagaag ctgaactcac 500

gccgagacct gcaggagtgg tgccaggtgc ttgaagtaac aagtttaaaa 550

tgttcagaga caatggaatg gaatctatta ggcaagaaca ggacattatg 600

aaataaggac aggtggactt ccaaaaacac aagtagaaat tctaacaatg 650

aaatatatta caggcaggtc acccactaac caaacaactg aagcgagagc 700

tgtggtcttg cttggtctca cagtgggcac agcggtaggc ggtcagtcat 750

gttgctgaac gacggagggt aaactcccca gccccaagaa aacctgtgtt 800

256

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ggaagtaaca acaacctccc tgctcctggc accagccgtt ttggtcatgg 850

tgggccagct gcaaagcgtc ttccattctc tgggcagtgg tggccccgag 900

gctgtggcct ctcagggggt ttctgtggac acgggcagca gagtgtgtcc 950

aggccagccc ccaagaatgc cctgctcctg acagcttggc caacccctgg 1000

tcagggcaga gggagttggg tgggtcaggc tctgggctca cctccatctc 1050

cagagcatcc cctgcctgca gttgtggcaa gaacgcccag ctcagaatga 1100

acacacccca ccaagagcct ccttgttcat aaccacaggt taccctacaa 1150

accactgtcc ccacacaacc ctggggatgt tttaaaacac acacctctaa 1200

cgcatatctt acagtcactg ttgtcttgcc tgagggttga attttttta 1250

atgaaagtgc aatgaaaatc actggattaa atcctacgga cacagagctg 1300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1332
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<210> 270
<211> 142
<212> PRT
<213> Homo sapiens

<400> 270
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Met Asn Thr Trp Leu Leu Phe Leu Pro Leu Phe Pro Val Gln Val
  1               5                  10                  15

Gln Thr Leu Ile Val Val Ile Ile Gly Met Leu Val Leu Leu Leu
                 20                  25                  30

Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu Leu Ile Phe His
                 35                  40                  45

Ile Tyr Leu Ser Met Ser Pro Thr Leu Ser Pro Arg Ser Pro Gln
                 50                  55                  60

Gly Trp Val Val Arg Ala Ala His Leu Thr Pro Leu Leu Glu Tyr
                 65                  70                  75

Val Pro Asn Pro Glu Pro Pro Thr Pro Gly Ala Arg Val Phe Val
                 80                  85                  90

Pro Arg Val Arg Met Cys Ser Gly Ser Ala Ser Pro Arg Ser Glu
                 95                 100                 105

Ile Met Asp Lys Lys Gly Lys Ser Gln Glu Glu Ile Lys Ser Met
                110                 115                 120

Arg Thr Gln Gln Ala Gln Gln Glu Ala Glu Leu Thr Pro Arg Pro
                125                 130                 135

Ala Gly Val Val Pro Gly Ala
                140
```

257

<210> 271
<211> 1484
<212> DNA
<213> Homo sapiens

<400> 271
ggagtgcaga tggcatcctt cggttcttcc agacaagctg caagacgctg 50

accatggcca agatggagct ctcgaaggcc ttctctggcc agcggacact 100

cctatctgcc atcctcagca tgctatcact cagcttctcc acaacatccc 150

tgctcagcaa ctactggttt gtgggcacac agaaggtgcc caagcccctg 200

tgcgagaaag gtctggcagc caagtgcttt gacatgccag tgtccctgga 250

tggagatacc aacacatcca cccaggaggt ggtacaatac aactgggaga 300

ctggggatga ccggttctcc ttccggagct ccggagtgg catgtggcta 350

tcctgtgagg aaactgtgga agaaccaggg gagaggtgcc gaagtttcat 400

tgaacttaca ccaccagcca agagaggtga aaaggacta ctggaatttg 450

ccacgttgca aggcccatgt caccccactc tccgatttgg agggaagcgg 500

ttgatggaga aggcttccct cccctcccct cccttggggc tttgtggcaa 550

aaatcctatg gttatccctg ggaacgcaga tcacctacat cggacttcaa 600

ttcatcagct tcctcctgct actaacagac ttgctactca ctgggaaccc 650

tgcctgtggg ctcaaactga gcgcctttgc tgctgtttcc tctgtcctgt 700

caggtctcct ggggatggtg gcccacatga tgtattcaca agtcttccaa 750

gcgactgtca acttgggtcc agaagactgg agaccacatg tttggaatta 800

tggctgggcc ttctacatgg cctggctctc cttcacctgc tgcatggcgt 850

cggctgtcac caccttcaac acgtacacca ggatggtgct ggagttcaag 900

tgcaagcata gtaagagctt caaggaaaac ccgaactgcc taccacatca 950

ccatcagtgt ttccctcggc ggctgtcaag tgcagccccc accgtgggtc 1000

ctttgaccag ctaccaccag tatcataatc agcccatcca ctctgtctct 1050

gagggagtcg acttctactc cgagctgcgg aacaagggat ttcaaagagg 1100

ggccagccag gagctgaaag aagcagttag gtcatctgta gaggaagagc 1150

agtgttagga gttaagcggg tttggggagt aggcttgagc cctaccttac 1200

acgtctgctg attatcaaca tgtgcttaag ccaacatccg tctcttgagc 1250

atggtttta gaggctacga ataaggctat gaataagggt tatctttaag 1300

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tcctaaggga ttcctgggtg ccactgctct cttttcctct acagctccat 1350

cttgtttcac ccaccccaca tctcacacat ccagaattcc cttctttact 1400

gatagtttct gtgccaggtt ctgggctaaa ccatggagat aaaaagaaga 1450

gtaaaataca cttcccgacc ttaaggatct gaaa 1484
```

<210> 272
<211> 285
<212> PRT
<213> Homo sapiens

<400> 272
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Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr
 1               5                  10                  15

Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr
                20                  25                  30

Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val
                35                  40                  45

Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp
                50                  55                  60

Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu
                65                  70                  75

Val Val Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe
                80                  85                  90

Arg Ser Phe Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val
                95                  100                 105

Glu Glu Pro Gly Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro
                110                 115                 120

Pro Ala Lys Arg Gly Glu Lys Gly Leu Leu Glu Phe Ala Thr Leu
                125                 130                 135

Gln Gly Pro Cys His Pro Thr Leu Arg Phe Gly Gly Lys Arg Leu
                140                 145                 150

Met Glu Lys Ala Ser Leu Pro Ser Pro Leu Gly Leu Cys Gly
                155                 160                 165

Lys Asn Pro Met Val Ile Pro Gly Asn Ala Asp His Leu His Arg
                170                 175                 180

Thr Ser Ile His Gln Leu Pro Pro Ala Thr Asn Arg Leu Ala Thr
                185                 190                 195

His Trp Glu Pro Cys Leu Trp Ala Gln Thr Glu Arg Leu Cys Cys
                200                 205                 210

Cys Phe Leu Cys Pro Val Arg Ser Pro Gly Asp Gly Gly Pro His
                215                 220                 225
```

259

```
Asp Val Phe Thr Ser Leu Pro Ser Asp Cys Gln Leu Gly Ser Arg
            230                 235             240

Arg Leu Glu Thr Thr Cys Leu Glu Leu Trp Leu Gly Leu Leu His
            245                 250             255

Gly Leu Ala Leu Leu His Leu Leu His Gly Val Gly Cys His His
            260                 265             270

Leu Gln His Val His Gln Asp Gly Ala Gly Val Gln Val Gln Ala
            275                 280             285
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<210> 273
<211> 1158
<212> DNA
<213> Homo sapiens

<400> 273
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aactggaagg aaagaaagaa aggtcagctt tggcccagat gtggttaccc 50

cttggtctcc tgtctttatg tctttctcct cttcctattc tgtcatctcc 100

ctcacttaag tctcaggcct gtcagcagct cctgtggaca ttgccatccc 150

ctctggtagc cttcagagca aacaggacaa cctatgttat ggatgtttcc 200

accaaccagg gtagtggcat ggagcaccgt aaccatctgt gcttctgtga 250

tctctatgac agagccactt ctccacctct gaaatgttcc ctgctctgaa 300

atctggcatg agatggcaca ggtgaccacg cagaagccac cagaatcttg 350

cctgccctat tcctcctccc aagtctgttc tcttattgtc aacctcagca 400

caacaggctg gcgccaatgg cattacagag aaagcaatct gtgtggctag 450

tgggcagatt accatgcaag ccccaggaga aatggaggag ctttgtagcc 500

acctccctgt cagccagtat taacatgtcc ccttccccct gccccgccgt 550

agattcagga cattcgcccc tgtgtgccac caaaccagga ctttcccctt 600

ggcttggcat ccctggctct ctcctggtac ccagcaagac gtctgttcca 650

gggcagtgta gcatctttca agctccgtta ctatggcgat ggccatgatg 700

ttacaatccc acttgcctga ataatcaagt gggaagggga agcagaggga 750

aatggggcca tgtgaatgca gctgctctgt tctccctacc ctgaggaaaa 800

accaaaggga agcaacagga acttctgcaa ctggttttta tcggaaagat 850

catcctgcct gcagatgctg ttgaaggggc acaagaaatg tagctggaga 900

agattgatga aagtgcaggt gtgtaaggaa atagaacagt ctgctgggag 950

tcagacctgg aattctgatt ccaaactctt tattactttg ggaagtcact 1000
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cagcctcccc gtagccatct ccagggtgac ggaacccagt gtattacctg 1050

ctggaaccaa ggaaactaac aatgtaggtt actagtgaat accccaatgg 1100

tttctccaat tatgcccatg ccaccaaaac aataaaacaa aattctctaa 1150

cactgaaa 1158

<210> 274
<211> 86
<212> PRT
<213> Homo sapiens

<400> 274
Met Trp Leu Pro Leu Gly Leu Leu Ser Leu Cys Leu Ser Pro Leu
  1   5   10   15

Pro Ile Leu Ser Ser Pro Ser Leu Lys Ser Gln Ala Cys Gln Gln
                 20   25   30

Leu Leu Trp Thr Leu Pro Ser Pro Leu Val Ala Phe Arg Ala Asn
                 35   40   45

Arg Thr Thr Tyr Val Met Asp Val Ser Thr Asn Gln Gly Ser Gly
                 50   55   60

Met Glu His Arg Asn His Leu Cys Phe Cys Asp Leu Tyr Asp Arg
                 65   70   75

Ala Thr Ser Pro Pro Leu Lys Cys Ser Leu Leu
                 80   85

<210> 275
<211> 2694
<212> DNA
<213> Homo sapiens

<400> 275
gtagcgcgtc ttgggtctcc cggctgccgc tgctgccgcc gccgcctcgg 50

gtcgtggagc caggagcgac gtcaccgcca tggcaggcat caaagctttg 100

attagtttgt cctttggagg agcaatcgga ctgatgtttt tgatgcttgg 150

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261

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acatttttga gataaggttt ttatttatgt ttattattgt tagagtgagt 1250

tgcaatgtgg gaagaaatga cattgaaatt ccagtttttg aatcctgttt 1300

ctatttataa gtgaaatttg tgatctccta tcaacctttc atgttttacc 1350

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262

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<211> 131
<212> PRT
<213> Homo sapiens

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Ile Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr
                20   25   30

Asn Lys Tyr Trp Pro Leu Phe Val Leu Phe Phe Tyr Ile Leu Ser
                35   40   45

Pro Ile Pro Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp
                50   55   60

Ala Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr
                65   70   75

Gly Ile Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg
                80   85   90

Ala His Leu Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly
                95   100   105

Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe

263

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<212> DNA
<213> Homo sapiens

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  ggctgtttcc gcggagtaaa aggtggcgcc ggtcagtggt cgtttccaat 300

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  ctgcccaaca ccaccttccg gcccatgccc aacctgcgca gcgtggacct 1150

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264

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265

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266

gtca 4104

<210> 278
<211> 522
<212> PRT
<213> Homo sapiens

<400> 278
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Arg Pro Ser Gly Val Val Leu Cys Leu Leu Gly Ala Cys Phe Gln
                20                  25                  30

Met Leu Pro Ala Ala Pro Ser Gly Cys Pro Gln Leu Cys Arg Cys
                35                  40                  45

Glu Gly Arg Leu Leu Tyr Cys Glu Ala Leu Asn Leu Thr Glu Ala
                50                  55                  60

Pro His Asn Leu Ser Gly Leu Leu Gly Leu Ser Leu Arg Tyr Asn
                65                  70                  75

Ser Leu Ser Glu Leu Arg Ala Gly Gln Phe Thr Gly Leu Met Gln
                80                  85                  90

Leu Thr Trp Leu Tyr Leu Asp His Asn His Ile Cys Ser Val Gln
                95                 100                 105

Gly Asp Ala Phe Gln Lys Leu Arg Arg Val Lys Glu Leu Thr Leu
               110                 115                 120

Ser Ser Asn Gln Ile Thr Gln Leu Pro Asn Thr Thr Phe Arg Pro
               125                 130                 135

Met Pro Asn Leu Arg Ser Val Asp Leu Ser Tyr Asn Lys Leu Gln
               140                 145                 150

Ala Leu Ala Pro Asp Leu Phe His Gly Leu Arg Lys Leu Thr Thr
               155                 160                 165

Leu His Met Arg Ala Asn Ala Ile Gln Phe Val Pro Val Arg Ile
               170                 175                 180

Phe Gln Asp Cys Arg Ser Leu Lys Phe Leu Asp Ile Gly Tyr Asn
               185                 190                 195

Gln Leu Lys Ser Leu Ala Arg Asn Ser Phe Ala Gly Leu Phe Lys
               200                 205                 210

Leu Thr Glu Leu His Leu Glu His Asn Asp Leu Val Lys Val Asn
               215                 220                 225

Phe Ala His Phe Pro Arg Leu Ile Ser Leu His Ser Leu Cys Leu
               230                 235                 240

Arg Arg Asn Lys Val Ala Ile Val Val Ser Ser Leu Asp Trp Val
               245                 250                 255
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267

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Trp Asn Leu Glu Lys Met Asp Leu Ser Gly Asn Glu Ile Glu Tyr
            260                 265                 270

Met Glu Pro His Val Phe Glu Thr Val Pro His Leu Gln Ser Leu
            275                 280                 285

Gln Leu Asp Ser Asn Arg Leu Thr Tyr Ile Glu Pro Arg Ile Leu
            290                 295                 300

Asn Ser Trp Lys Ser Leu Thr Ser Ile Thr Leu Ala Gly Asn Leu
            305                 310                 315

Trp Asp Cys Gly Arg Asn Val Cys Ala Leu Ala Ser Trp Leu Ser
            320                 325                 330

Asn Phe Gln Gly Arg Tyr Asp Gly Asn Leu Gln Cys Ala Ser Pro
            335                 340                 345

Glu Tyr Ala Gln Gly Glu Asp Val Leu Asp Ala Val Tyr Ala Phe
            350                 355                 360

His Leu Cys Glu Asp Gly Ala Glu Pro Thr Ser Gly His Leu Leu
            365                 370                 375

Ser Ala Val Thr Asn Arg Ser Asp Leu Gly Pro Pro Ala Ser Ser
            380                 385                 390

Ala Thr Thr Leu Ala Asp Gly Gly Glu Gly Gln His Asp Gly Thr
            395                 400                 405

Phe Glu Pro Ala Thr Val Ala Leu Pro Gly Gly Glu His Ala Glu
            410                 415                 420

Asn Ala Val Gln Ile His Lys Val Val Thr Gly Thr Met Ala Leu
            425                 430                 435

Ile Phe Ser Phe Leu Ile Val Val Leu Val Leu Tyr Val Ser Trp
            440                 445                 450

Lys Cys Phe Pro Ala Ser Leu Arg Gln Leu Arg Gln Cys Phe Val
            455                 460                 465

Thr Gln Arg Arg Lys Gln Lys Gln Lys Gln Thr Met His Gln Met
            470                 475                 480

Ala Ala Met Ser Ala Gln Glu Tyr Tyr Val Asp Tyr Lys Pro Asn
            485                 490                 495

His Ile Glu Gly Ala Leu Val Ile Ile Asn Glu Tyr Gly Ser Cys
            500                 505                 510

Thr Cys His Gln Gln Pro Ala Arg Glu Cys Glu Val
            515                 520

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<212>  DNA
<213>  Artificial Sequence


268
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<220>
<223> Synthetic oligonucleotide probe

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<210> 280
<211> 709
<212> DNA
<213> Homo sapiens

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 ccggcggcgc cgttgagttc ccggcggaca agatggtgtc agtcctggtg 200

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<210> 281
<211> 229
<212> PRT
<213> Homo sapiens

<400> 281
 Met Gly Val Leu Gly Arg Val Leu Leu Trp Leu Gln Leu Cys Ala
  1   5   10   15

 Leu Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe
                 20   25   30

 Asp Val Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly
                 35   40   45

 Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val

269

                    50   55   60

Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly
                65   70   75

Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser Asp Val
                80   85   90

Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe Arg
                95   100   105

Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser
               110   115   120

Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val
               125   130   135

Pro Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe
               140   145   150

Arg Val Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser
               155   160   165

Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala
               170   175   180

Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro
               185   190   195

Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly
               200   205   210

Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala Ala
               215   220   225

Leu Leu Gln Pro

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<211> 644
<212> DNA
<213> Homo sapiens

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 cctttccttc ataccatttg caagggatgc tgtgaagaag tgttttgccg 250

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270

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cagtagcaca ggatgagaag tgggttctgt atcttgtgga gtggaatctt 500

cctcatgtac ctgtttcctc tctggatgtt gtcccactga attcccatga 550

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 644

<210> 283
<211> 77
<212> PRT
<213> Homo sapiens

<400> 283
Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg
1   5   10   15

Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr Leu
                20   25   30

Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
                35   40   45

Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe
                50   55   60

Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys
                65   70   75

Leu Ala

<210> 284
<211> 2623
<212> DNA
<213> Homo sapiens

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ccagatagat tatcttacac tgaactgatc aagtactttg aaaatgactt 250

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tggattccgt tgggattact tatataaagt tccaacgccc cattttcatt 400

271

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gaatcatggg attgttgcaa atgatatgtt tgatcctatt cggaacaaat 550

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agccatgtgg cccggaacag atgtaaaaat acataagcgc tttcctactc 700

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tcatggggcc tgtcatttca gatattgaca agaagttagg atatctcata 900

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gcagccatct tgccaaaaga aggtaaattt gatgaagtct atgaagcact 1100

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tccacagatt tgtacccact actatgccac ctcctcaata tcactgccat 1400

gccacacaat ggatcattct ggaatgtcca ggatctgctc aattcagcaa 1450

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agcatttaat tcacagtcaa atacctgcct tacaagatat gcatgctgaa 1650

atagctcaac cattattaca agcctaatgt tactttgaag tggatttgca 1700

tattgaagtg gagattccat aattatgtca gtgtttaaag gtttcaaatt 1750

ctgggaaacc agttccaaac atctgcagaa accattaagc agttacatat 1800

ttaggtatac acacacacac acacacacac atacacacac acggaccaaa 1850

272

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cactgtagca tagggataga taagatcctg ctttatttgg acttggcgca 1950

gataatgtat atatttagca actttgcact atgtaaagta ccttatatat 2000

tgcactttaa atttctctcc tgatgggtac tttaatttga aatgcacttt 2050

atggacagtt atgtcttata acttgattga aaatgacaac tttttgcacc 2100

catgtcacag aatacttgtt acgcattgtt caaactgaag gaaatttcta 2150

ataatcccga ataatgaaca tagaaatcta tctccataaa ttgagagaag 2200

aagaaggtga taagtgttga aaattaaatg tgataacctt gaaccttga 2250

attttggaga tgtattccca acagcagaat gcaactgtgg gcatttcttg 2300

tcttatttct ttccagagaa cgtggttttc atttattttt ccctcaaaag 2350

agagtcaaat actgacagat tcgttctaaa tatattgttt ctgtcataaa 2400

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aagacaccat gaatatactt ttcttctata tagttcagca atggcctgaa 2500

tagaagcaac caggcaccat ctcagcaatg ttttctcttg tttgtaatta 2550

tttgctcctt tgaaaattaa atcactatta attacattaa aaatcaaatt 2600

ggataaaaaa aaaaaaaaaa aaa 2623
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<210> 285
<211> 477
<212> PRT
<213> Homo sapiens

<400> 285
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Met Thr Ser Lys Phe Ile Leu Val Ser Phe Ile Leu Ala Ala Leu
  1               5                  10                  15

Ser Leu Ser Thr Thr Phe Ser Leu Gln Leu Asp Gln Gln Lys Val
             20                  25                  30

Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asp Tyr Leu Tyr Lys
             35                  40                  45

Val Pro Thr Pro His Phe His Tyr Ile Met Lys Tyr Gly Val His
             50                  55                  60

Val Lys Gln Val Thr Asn Val Phe Ile Thr Lys Thr Tyr Pro Asn
             65                  70                  75

His Tyr Thr Leu Val Thr Gly Leu Phe Ala Glu Asn His Gly Ile
             80                  85                  90

Val Ala Asn Asp Met Phe Asp Pro Ile Arg Asn Lys Ser Phe Ser
             95                 100                 105
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273

Leu Asp His Met Asn Ile Tyr Asp Ser Lys Phe Trp Glu Glu Ala
                    110   115   120

Thr Pro Ile Trp Ile Thr Asn Gln Arg Ala Gly His Thr Ser Gly
                    125   130   135

Ala Ala Met Trp Pro Gly Thr Asp Val Lys Ile His Lys Arg Phe
                    140   145   150

Pro Thr His Tyr Met Pro Tyr Asn Glu Ser Val Ser Phe Glu Asp
                    155   160   165

Arg Val Ala Lys Ile Val Glu Trp Phe Thr Ser Lys Glu Pro Ile
                    170   175   180

Asn Leu Gly Leu Leu Tyr Trp Glu Asp Pro Asp Asp Met Gly His
                    185   190   195

His Leu Gly Pro Asp Ser Pro Leu Met Gly Pro Val Ile Ser Asp
                    200   205   210

Ile Asp Lys Lys Leu Gly Tyr Leu Ile Gln Met Leu Lys Lys Ala
                    215   220   225

Lys Leu Trp Asn Thr Leu Asn Leu Ile Ile Thr Ser Asp His Gly
                    230   235   240

Met Thr Gln Cys Ser Glu Glu Arg Leu Ile Glu Leu Asp Gln Tyr
                    245   250   255

Leu Asp Lys Asp His Tyr Thr Leu Ile Asp Gln Ser Pro Val Ala
                    260   265   270

Ala Ile Leu Pro Lys Glu Gly Lys Phe Asp Glu Val Tyr Glu Ala
                    275   280   285

Leu Thr His Ala His Pro Asn Leu Thr Val Tyr Lys Lys Glu Asp
                    290   295   300

Val Pro Glu Arg Trp His Tyr Lys Tyr Asn Ser Arg Ile Gln Pro
                    305   310   315

Ile Ile Ala Val Ala Asp Glu Gly Trp His Ile Leu Gln Asn Lys
                    320   325   330

Ser Asp Asp Phe Leu Leu Gly Asn His Gly Tyr Asp Asn Ala Leu
                    335   340   345

Ala Asp Met His Pro Ile Phe Leu Ala His Gly Pro Ala Phe Arg
                    350   355   360

Lys Asn Phe Ser Lys Glu Ala Met Asn Ser Thr Asp Leu Tyr Pro
                    365   370   375

Leu Leu Cys His Leu Leu Asn Ile Thr Ala Met Pro His Asn Gly
                    380   385   390

Ser Phe Trp Asn Val Gln Asp Leu Leu Asn Ser Ala Met Pro Arg

274

Val Val Pro Tyr Thr Gln Ser Thr Ile Leu Leu Pro Gly Ser Val
                410   415   420

Lys Pro Ala Glu Tyr Asp Gln Glu Gly Ser Tyr Pro Tyr Phe Ile
                425   430   435

Gly Val Ser Leu Gly Ser Ile Ile Val Ile Val Phe Phe Val Ile
                440   445   450

Phe Ile Lys His Leu Ile His Ser Gln Ile Pro Ala Leu Gln Asp
                455   460   465

Met His Ala Glu Ile Ala Gln Pro Leu Leu Gln Ala
                470   475

<210> 286
<211> 1337
<212> DNA
<213> Homo sapiens

<400> 286
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 agggaggtga agaaaccaag acgcagagag gccaagcccc ttgccttggg 150

 tcacacagcc aaaggaggca gagccagaac tcacaaccag atccagaggc 200

 aacagggaca tggccacctg ggacgaaaag gcagtcaccc gcaggccaa 250

 ggtggctccc gctgagagga tgagcaagtt cttaaggcac ttcacggtcg 300

 tgggagacga ctaccatgcc tggaacatca actacaagaa atgggagaat 350

 gaagaggagg aggaggagga ggagcagcca ccacccacac cagtctcagg 400

 cgaggaaggc agagctgcag cccctgacgt tgcccctgcc cctggccccg 450

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ctctcacaca gccaccgtga aagtcctgga gtaaaatgtg ctgtgtacag 1100

aagagagaga aggaagcagg ctggcatgtt cactgggctg gtgttacgac 1150

agagaacctg acagtcactg gccagttatc acttcagatt acaaatcaca 1200

cagagcatct gcctgttttc aatcacaaga gaacaaaacc aaaatctata 1250

aagatattct gaaaatatga cagaatttga caaataaaag cataaacgtg 1300

taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1337
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<210> 287
<211> 255
<212> PRT
<213> Homo sapiens

<400> 287

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Met Ala Thr Trp Asp Glu Lys Ala Val Thr Arg Arg Ala Lys Val
  1               5                  10                  15

Ala Pro Ala Glu Arg Met Ser Lys Phe Leu Arg His Phe Thr Val
                 20                  25                  30

Val Gly Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp
                 35                  40                  45

Glu Asn Glu Glu Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr
                 50                  55                  60

Pro Val Ser Gly Glu Glu Gly Arg Ala Ala Ala Pro Asp Val Ala
                 65                  70                  75

Pro Ala Pro Gly Pro Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly
                 80                  85                  90

Met Leu Arg Lys Leu Phe Ser Ser His Arg Phe Gln Val Ile Ile
                 95                 100                 105

Ile Cys Leu Val Val Leu Asp Ala Leu Leu Val Leu Ala Glu Leu
                110                 115                 120

Ile Leu Asp Leu Lys Ile Ile Gln Pro Asp Lys Asn Asn Tyr Ala
                125                 130                 135

Ala Met Val Phe His Tyr Met Ser Ile Thr Ile Leu Val Phe Phe
                140                 145                 150

Met Met Glu Ile Ile Phe Lys Leu Phe Val Phe Arg Leu Ser Ser
                155                 160                 165

Phe Thr Thr Ser Leu Arg Ser Trp Met Pro Val Val Val Val Val
```

276

Ser Phe Ile Leu Asp Ile Val Leu Leu Phe Gln Glu His Gln Phe
                185   190   195

Glu Ala Leu Gly Leu Leu Ile Leu Leu Arg Leu Trp Arg Val Ala
                200   205   210

Arg Ile Ile Asn Gly Ile Ile Ile Ser Val Lys Thr Arg Ser Glu
                215   220   225

Arg Gln Leu Leu Arg Leu Lys Gln Met Asn Val Gln Leu Ala Ala
                230   235   240

Lys Ile Gln His Leu Glu Phe Ser Cys Ser Glu Lys Pro Leu Asp
                245   250   255

<210> 288
<211> 3334
<212> DNA
<213> Homo sapiens

<400> 288
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 cccagaccga gttccagtac tttgagtcga aggggctccc tgccgagctg 150

 aagtccattt tcaagctcag tgtcttcatc ccctcccagg aattctccac 200

 ctaccgccag tggaagcaga aaattgtaca agctggagat aaggaccttg 250

 atgggcagct agactttgaa gaatttgtcc attatctcca agatcatgag 300

 aagaagctga ggctggtgtt taagattttg gacaaaaaga atgatggacg 350

 cattgacgcg caggagatca tgcagtccct gcgggacttg ggagtcaaga 400

 tatctgaaca gcaggcagaa aaaattctca gagcatgga taaaaacggc 450

 acgatgacca tcgactggaa cgagtggaga gactaccacc tcctccaccc 500

 cgtggaaaac atccccgaga tcatcctcta ctggaagcat tccacgatct 550

 ttgatgtggg tgagaatcta acggtcccgg atgagttcac agtggaggag 600

 aggcagacgg ggatgtggtg gagacacctg gtggcaggag gtggggcagg 650

 ggccgtatcc agaacctgca cggcccccct ggacaggctc aaggtgctca 700

 tgcaggtcca tgcctcccgc agcaacaaca tgggcatcgt tggtggcttc 750

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277

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gccagtactc aggaatgctg gactgcgcca ggaggatcct ggccagagag 1050

ggggtggccg ccttctacaa aggctatgtc cccaacatgc tgggcatcat 1100

cccctatgcc ggcatcgacc ttgcagtcta cgagacgctc aagaatgcct 1150

ggctgcagca ctatgcagtg aacagcgcgg accccggcgt gtttgtgctc 1200

ctggcctgtg caccatgtc cagtacctgt ggccagctgg ccagctaccc 1250

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ggggccttcg ggctgtacag ggggctggcc cccaacttca tgaaggtcat 1400

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tgggcgtgca gtcgcggtga cggggggagg gccgcccggc agtggactcg 1500

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tgccaacact aagctgtctc gagccaagct gtgaaaaccc tagacgcacc 1600

cgcagggagg gtggggagag ctggcaggcc cagggcttgt cctgctgacc 1650

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tggggaggga aggaaaaggt gttggaggcc ttaattatgg actgttggga 2350

278

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aatgcaaaaa ttgttatata tgaacatata actggagtcg tcaaaaagca 3200

aattaagaaa gaattggacg ttagaagttg tcatttaaag cagccttcta 3250

ataaagttgt ttcaaagctg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 3334
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<210> 289
<211> 469
<212> PRT
<213> Homo sapiens

<400> 289

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Met Leu Cys Leu Cys Leu Tyr Val Pro Val Ile Gly Glu Ala Gln
1               5                   10                  15

Thr Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu
                20                  25                  30

Lys Ser Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe
                35                  40                  45

Ser Thr Tyr Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp
                50                  55                  60
```

Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr
                65   70   75

Leu Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ile Leu
                80   85   90

Asp Lys Lys Asn Asp Gly Arg Ile Asp Ala Gln Glu Ile Met Gln
                95   100   105

Ser Leu Arg Asp Leu Gly Val Lys Ile Ser Glu Gln Gln Ala Glu
               110   115   120

Lys Ile Leu Lys Ser Met Asp Lys Asn Gly Thr Met Thr Ile Asp
               125   130   135

Trp Asn Glu Trp Arg Asp Tyr His Leu Leu His Pro Val Glu Asn
               140   145   150

Ile Pro Glu Ile Ile Leu Tyr Trp Lys His Ser Thr Ile Phe Asp
               155   160   165

Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe Thr Val Glu Glu
               170   175   180

Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala Gly Gly Gly
               185   190   195

Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp Arg Leu
               200   205   210

Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met Gly
               215   220   225

Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Arg
               230   235   240

Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro
               245   250   255

Glu Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Ile Lys Arg Leu
               260   265   270

Val Gly Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val
               275   280   285

Ala Gly Ser Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro
               290   295   300

Met Glu Val Leu Lys Thr Arg Met Ala Leu Arg Lys Thr Gly Gln
               305   310   315

Tyr Ser Gly Met Leu Asp Cys Ala Arg Arg Ile Leu Ala Arg Glu
               320   325   330

Gly Val Ala Ala Phe Tyr Lys Gly Tyr Val Pro Asn Met Leu Gly
               335   340   345

Ile Ile Pro Tyr Ala Gly Ile Asp Leu Ala Val Tyr Glu Thr Leu

280

Lys Asn Ala Trp Leu Gln His Tyr Ala Val Asn Ser Ala Asp Pro
                365   370   375

Gly Val Phe Val Leu Leu Ala Cys Gly Thr Met Ser Ser Thr Cys
                380   385   390

Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu Val Arg Thr Arg Met
                395   400   405

Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu Val Thr Met Ser
                410   415   420

Ser Leu Phe Lys His Ile Leu Arg Thr Glu Gly Ala Phe Gly Leu
                425   430   435

Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro Ala Val
                440   445   450

Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu Gly
                455   460   465

Val Gln Ser Arg

<210> 290
<211> 1658
<212> DNA
<213> Homo sapiens

<400> 290
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 atttcaggga gacactccat cacagtcact actgtcgcct cagctgggaa 200

 cattggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac 250

 tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggcttggtc 300

 catgagttca agaaggcaa agatgagctg tcggagcagg atgaaatgtt 350

 cagaggccgg acagcagtgt ttgctgatca agtgatagtt ggcaatgcct 400

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 tatatcatca cttctaaagg caaggggaat gctaaccttg agtataaaac 500

 tggagccttc agcatgccgg aagtgaatgt ggactataat gccagctcag 550

 agaccttgcg gtgtgaggct ccccgatggt tcccccagcc cacagtggtc 600

 tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 650

cagctttgag ctgaactctg agaatgtgac catgaaggtt gtgtctgtgc 700

tctacaatgt tacgatcaac aacacatact cctgtatgat tgaaaatgac 750

attgccaaag caacagggga tatcaaagtg acagaatcgg agatcaaaag 800

gcggagtcac ctacagctgc taaactcaaa ggcttctctg tgtgtctctt 850

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tgtaatgttg ctctgaggaa gcccctggaa agtctatccc aacatatcca 1350

catcttatat tccacaaatt aagctgtagt atgtaccccta agacgctgct 1400

aattgactgc cacttcgcaa ctcaggggcg gctgcatttt agtaatgggt 1450

caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 1500

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ttaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650

aaaaaaaa 1658

<210> 291
<211> 282
<212> PRT
<213> Homo sapiens

<400> 291
Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile
1   5   10   15

Ile Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly
                20   25   30

Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala
                35   40   45

Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro

282

Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly
                65   70   75

Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu
                80   85   90

Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala
                95   100   105

Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val
                110   115   120

Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser
                125   130   135

Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe
                140   145   150

Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr
                155   160   165

Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln Pro Thr Val Val
                170   175   180

Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser Glu Val Ser
                185   190   195

Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys Val
                200   205   210

Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys
                215   220   225

Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
                230   235   240

Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn
                245   250   255

Ser Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp
                260   265   270

Ala Leu Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
                275   280

<210> 292
<211> 1484
<212> DNA
<213> Homo sapiens

<400> 292
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 tgaagcgggc ctccgccggc ctgcagcggg ttcatgagcc gacctgggcc 150

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gatgcccttt ctcctcaacc agtgtggatc ccttctctat tacctcacct 250

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aatttcactc tgcatcacaa gctcagtgag taagacccag gggcaacagt 750

ctaccctttg agtgggccga acccacttcc agctctgctg cctccaggaa 800

gcccctgggc catgaagtgc tggcagtgag cggatggacc tagcacttcc 850

cctctctggc cttagcttcc tcctctctta tggggataac agctacctca 900

tggatcacaa taagagaaca agagtgaaag agttttgtaa ccttcaagtg 950

ctgttcagct gcggggattt agcacaggag actctacgct caccctcagc 1000

aacctttctg ccccagcagc tctcttcctg ctaacatctc aggctcccag 1050

cccagccacc attactgtgg cctgatctgg actatcatgg tggcaggttc 1100

catggactgc agaactccag ctgcatggaa agggccagct gcagactttg 1150

agccagaaat gcaaacggga ggcctctggg actcagtcag agcgctttgg 1200

ctgaatgagg ggtggaaccg agggaagaag gtgcgtcgga gtggcagatg 1250

caggaaatga gctgtctatt agccttgcct gccccaccca tgaggtaggc 1300

agaaatcctc actgccagcc cctcttaaac aggtagagag ctgtgagccc 1350

cagcccacc tgactccagc acacctggcg agtagtagct gtcaataaat 1400

ctatgtaaac agacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1484

<210> 293
<211> 180
<212> PRT
<213> Homo sapiens
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<400> 293
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Met Ala Ala Ser Leu Gly Gln Val Leu Ala Leu Val Leu Val Ala
  1           5              10                   15

Ala Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ala
             20              25                   30

Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala Gln Gln Leu Leu
             35              40                   45

Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro
             50              55                   60

Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu
             65              70                   75

Ala Ser Thr Asp Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu
             80              85                   90

Ala Ile Ile Phe Thr Leu Ile Val Gly Lys Ala Leu Gly Glu Asp
             95             100                  105

Ile Gly Gly Lys Arg Lys Leu Asp Tyr Cys Glu Cys Gly Thr Gln
            110             115                  120

Leu Cys Gly Ser Arg His Thr Cys Val Ser Ser Phe Pro Glu Pro
            125             130                  135

Ile Ser Pro Glu Trp Val Arg Thr Arg Pro Phe Pro Ile Leu Pro
            140             145                  150

Phe Pro Leu Gln Leu Phe Cys Phe Leu Val Ala Ile Arg Val Pro
            155             160                  165

Phe Pro Trp Thr Val Trp Arg Lys Thr Glu Ala Gly Val Trp Asp
            170             175                  180
```

<210> 294
<211> 1164
<212> DNA
<213> Homo sapiens

<400> 294
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cttctgtagg acagtcacca ggccagatcc agaagcctct ctaggctcca  50

gctttctctg tggaagatga cagcaattat agcaggaccc tgccaggctg 100

tcgaaaagat tccgcaataa aactttgcca gtgggaagta cctagtgaaa 150

cggcctaaga tgccacttct tctcatgtcc caggcttgag gccctgtggt 200

ccccatcctt gggagaagtc agctccagca ccatgaaggg catcctcgtt 250

gctggtatca ctgcagtgct tgttgcagct gtagaatctc tgagctgcgt 300

gcagtgtaat tcatgggaaa aatcctgtgt caacagcatt gcctctgaat 350

gtccctcaca tgccaacacc agctgtatca gctcctcagc cagctcctct 400
```

285

```
ctagagacac cagtcagatt ataccagaat atgttctgct cagcggagaa 450

ctgcagtgag gagacacaca ttacagcctt cactgtccac gtgtctgctg 500

aagaacactt tcattttgta agccagtgct gccaaggaaa ggaatgcagc 550

aacaccagcg atgccctgga ccctcccctg aagaacgtgt ccagcaacgc 600

agagtgccct gcttgttatg aatctaatgg aacttcctgt cgtgggaagc 650

cctggaaatg ctatgaagaa gaacagtgtg tctttctagt tgcagaactt 700

aagaatgaca ttgagtctaa gagtctcgtg ctgaaaggct gttccaacgt 750

cagtaacgcc acctgtcagt tcctgtctgg tgaaaacaag actcttggag 800

gagtcatctt tcgaaagttt gagtgtgcaa atgtaaacag cttaaccccc 850

acgtctgcac caaccacttc ccacaacgtg ggctccaaag cttccctcta 900

cctcttggcc cttgccagcc tccttcttcg gggactgctg ccctgaggtc 950

ctggggctgc actttgccca gcaccccatt tctgcttctc tgaggtccag 1000

agcacccccct gcggtgctga caccctcttt ccctgctctg ccccgtttaa 1050

ctgcccagta agtgggagtc acaggtctcc aggcaatgcc gacagctgcc 1100

ttgttcttca ttattaaagc actggttcat tcactgccaa aaaaaaaaa 1150

aaaaaaaaaa aaaa 1164

<210> 295
<211> 237
<212> PRT
<213> Homo sapiens

<400> 295
 Met Lys Gly Ile Leu Val Ala Gly Ile Thr Ala Val Leu Val Ala
 1               5                  10                  15

 Ala Val Glu Ser Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys
                 20                  25                  30

 Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn
                 35                  40                  45

 Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro
                 50                  55                  60

 Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser
                 65                  70                  75

 Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu
                 80                  85                  90

 Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys
                 95                  100                 105
```

286

Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser
            110   115   120

Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser
            125   130   135

Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Gln Cys Val
            140   145   150

Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu
            155   160   165

Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe
            170   175   180

Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
            185   190   195

Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro
            200   205   210

Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu
            215   220   225

Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro
            230   235

<210> 296
<211> 1245
<212> DNA
<213> Homo sapiens

<400> 296
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 aggtaggagg cagggcttgc ctcactggcc accctcccaa ccccaagagc 100

 ccagccccat ggtccccgcc gccggcgcgc tgctgtgggt cctgctgctg 150

 aatctgggtc cccgggcggc ggggcccaa ggcctgaccc agactccgac 200

 cgaaatgcag cgggtcagtt tacgctttgg gggccccatg acccgcagct 250

 accggagcac cgcccggact ggtcttcccc ggaagacaag gataatccta 300

 gaggacgaga atgatgccat ggccgacgcc gaccgcctgg ctggaccagc 350

 ggctgccgag ctcttggccg ccacggtgtc caccggcttt agccggtcgt 400

 ccgccattaa cgaggaggat gggtcttcag aagaggggt tgtgattaat 450

 gccggaaagg atagcaccag cagagagctt cccagtgcga ctcccaatac 500

 agcgggggagt tccagcacga ggtttatagc caatagtcag gagcctgaaa 550

 tcaggctgac ttcaagcctg ccgcgctccc ccgggaggtc tactgaggac 600

 ctgccaggct cgcaggccac cctgagccag tggtccacac ctgggtctac 650

287

```
cccgagccgg tggccgtcac cctcacccac agccatgcca tctcctgagg 700

atctgcggct ggtgctgatg ccctggggcc cgtggcactg ccactgcaag 750

tcgggcacca tgagccggag ccggtctggg aagctgcacg gcctttccgg 800

gcgccttcga gttggggcgc tgagccagct ccgcacggag cacaagcctt 850

gcacctatca acaatgtccc tgcaaccgac ttcgggaaga gtgccccctg 900

gacacaagtc tctgtactga caccaactgt gcctctcaga gcaccaccag 950

taccaggacc accactaccc ccttccccac catccacctc agaagcagtc 1000

ccagcctgcc acccgccagc ccctgcccag ccctggcttt ttggaaacgg 1050

gtcaggattg gcctggagga tatttggaat agcctctctt cagtgttcac 1100

agagatgcaa ccaatagaca gaaaccagag gtaatggcca cttcatccac 1150

atgaggagat gtcagtatct caacctctct tgccctttca tcctagcac 1200

ccactagata ttttttagtac agaaaaacaa aactggaaaa cacaa 1245
```

<210> 297
<211> 341
<212> PRT
<213> Homo sapiens

<400> 297
```
Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn
  1               5                  10                  15

Leu Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro
                 20                  25                  30

Thr Glu Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr
                 35                  40                  45

Arg Ser Tyr Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr
                 50                  55                  60

Arg Ile Ile Leu Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp
                 65                  70                  75

Arg Leu Ala Gly Pro Ala Ala Ala Glu Leu Leu Ala Ala Thr Val
                 80                  85                  90

Ser Thr Gly Phe Ser Arg Ser Ser Ala Ile Asn Glu Glu Asp Gly
                 95                  100                 105

Ser Ser Glu Glu Gly Val Val Ile Asn Ala Gly Lys Asp Ser Thr
                 110                 115                 120

Ser Arg Glu Leu Pro Ser Ala Thr Pro Asn Thr Ala Gly Ser Ser
                 125                 130                 135

Ser Thr Arg Phe Ile Ala Asn Ser Gln Glu Pro Glu Ile Arg Leu
```

288

Thr Ser Ser Leu Pro Arg Ser Pro Gly Arg Ser Thr Glu Asp Leu
            155   160   165

Pro Gly Ser Gln Ala Thr Leu Ser Gln Trp Ser Thr Pro Gly Ser
            170   175   180

Thr Pro Ser Arg Trp Pro Ser Pro Ser Pro Thr Ala Met Pro Ser
            185   190   195

Pro Glu Asp Leu Arg Leu Val Leu Met Pro Trp Gly Pro Trp His
            200   205   210

Cys His Cys Lys Ser Gly Thr Met Ser Arg Ser Arg Ser Gly Lys
            215   220   225

Leu His Gly Leu Ser Gly Arg Leu Arg Val Gly Ala Leu Ser Gln
            230   235   240

Leu Arg Thr Glu His Lys Pro Cys Thr Tyr Gln Gln Cys Pro Cys
            245   250   255

Asn Arg Leu Arg Glu Glu Cys Pro Leu Asp Thr Ser Leu Cys Thr
            260   265   270

Asp Thr Asn Cys Ala Ser Gln Ser Thr Thr Ser Thr Arg Thr Thr
            275   280   285

Thr Thr Pro Phe Pro Thr Ile His Leu Arg Ser Ser Pro Ser Leu
            290   295   300

Pro Pro Ala Ser Pro Cys Pro Ala Leu Ala Phe Trp Lys Arg Val
            305   310   315

Arg Ile Gly Leu Glu Asp Ile Trp Asn Ser Leu Ser Ser Val Phe
            320   325   330

Thr Glu Met Gln Pro Ile Asp Arg Asn Gln Arg
            335   340

<210> 298
<211> 2692
<212> DNA
<213> Homo sapiens

<400> 298
 cccgggtcga cccacgcgtc cggggagaaa ggatggccgg cctggcggcg 50

 cggttggtcc tgctagctgg ggcagcggcg ctggcgagcg gctcccaggg 100

 cgaccgtgag ccggtgtacc gcgactgcgt actgcagtgc gaagagcaga 150

 actgctctgg gggcgctctg aatcacttcc gctcccgcca gccaatctac 200

 atgagtctag caggctggac ctgtcgggac gactgtaagt atgagtgtat 250

 gtgggtcacc gttgggctct acctccagga aggtcacaaa gtgcctcagt 300

```
tccatggcaa gtggccctc tcccggttcc tgttctttca agagccggca 350

tcggccgtgg cctcgtttct caatggcctg gccagcctgg tgatgctctg 400

ccgctaccgc accttcgtgc cagcctcctc ccccatgtac cacacctgtg 450

tggccttcgc ctgggtgtcc ctcaatgcat ggttctggtc cacagtcttc 500

cacaccaggg acactgacct cacagagaaa atggactact tctgtgcctc 550

cactgtcatc ctacactcaa tctacctgtg ctgcgtcagg accgtggggc 600

tgcagcaccc agctgtggtc agtgccttcc gggctctcct gctgctcatg 650

ctgaccgtgc acgtctccta cctgagcctc atccgcttcg actatggcta 700

caacctggtg gccaacgtgg ctattggcct ggtcaacgtg gtgtggtggc 750

tggcctggtg cctgtggaac cagcggcggc tgcctcacgt gcgcaagtgc 800

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gcaccatccc tgtccacgtc ctcttttttca gctttctgga agatgacagc 950

ctgtacctgc tgaaggaatc agaggacaag ttcaagctgg actgaagacc 1000

ttggagcgag tctgccccag tggggatcct gcccccgccc tgctggcctc 1050

ccttctcccc tcaacccttg agatgatttt ctcttttcaa cttcttgaac 1100

ttggacatga aggatgtggg cccagaatca tgtggccagc ccacccctg 1150

ttggccctca ccagccttgg agtctgttct agggaaggcc tcccagcatc 1200

tgggactcga gagtgggcag cccctctacc tcctggagct gaactggggt 1250

ggaactgagt gtgttcttag ctctaccggg aggacagctg cctgtttcct 1300

ccccaccagc ctcctcccca catccccagc tgcctggctg ggtcctgaag 1350

ccctctgtct acctgggaga ccagggacca caggccttag ggatacaggg 1400

ggtccccttc tgttaccacc ccccaccctc ctccaggaca ccactaggtg 1450

gtgctggatg cttgttcttt ggccagccaa ggttcacggc gattctcccc 1500

atgggatctt gagggaccaa gctgctggga ttgggaagga gtttcaccct 1550

gaccgttgcc ctagccaggt tcccaggagg cctcaccata ctccctttca 1600

gggccagggc tccagcaagc ccagggcaag gatcctgtgc tgctgtctgg 1650

ttgagagcct gccaccgtgt gtcgggagtg tgggccaggc tgagtgcata 1700

ggtgacaggg ccgtgagcat gggcctgggt gtgtgtgagc tcaggcctag 1750
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290

```
gtgcgcagtg tggagacggg tgttgtcggg gaagaggtgt ggcttcaaag 1800

tgtgtgtgtg caggggggtgg gtgtgttagc gtgggttagg ggaacgtgtg 1850

tgcgcgtgct ggtgggcatg tgagatgagt gactgccggt gaatgtgtcc 1900

acagttgaga ggttggagca ggatgaggga atcctgtcac catcaataat 1950

cacttgtgga gcgccagctc tgcccaagac gccacctggg cggacagcca 2000

ggagctctcc atggccaggc tgcctgtgtg catgttccct gtctggtgcc 2050

cctttgcccg cctcctgcaa acctcacagg gtccccacac aacagtgccc 2100

tccagaagca gcccctcgga ggcagaggaa ggaaaatggg gatggctggg 2150

gctctctcca tcctcctttt ctccttgcct tcgcatggct ggccttcccc 2200

tccaaaacct ccattcccct gctgccagcc cctttgccat agcctgattt 2250

tggggaggag gaaggggcga tttgagggag aaggggagaa agcttatggc 2300

tgggtctggt ttcttccctt cccagagggt cttactgttc cagggtggcc 2350

ccagggcagg caggggccac actatgcctg tgccctggta aaggtgaccc 2400

ctgccattta ccagcagccc tggcatgttc ctgccccaca ggaatagaat 2450

ggagggagct ccagaaactt tccatcccaa aggcagtctc cgtggttgaa 2500

gcagactgga tttttgctct gccctgacc ccttgtccct ctttgaggga 2550

ggggagctat gctaggactc caacctcagg gactcgggtg gcctgcgcta 2600

gcttcttttg atactgaaaa cttttaaggt gggagggtgg caagggatgt 2650

gcttaataaa tcaattccaa gcctcaaaaa aaaaaaaaaa aa 2692
```

<210> 299
<211> 320
<212> PRT
<213> Homo sapiens

<400> 299

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Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala
 1               5                  10                  15

Ala Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg
                20                  25                  30

Asp Cys Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala
                35                  40                  45

Leu Asn His Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala
                50                  55                  60

Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val
                65                  70                  75
```

291

```
Thr Val Gly Leu Tyr Leu Gln Glu Gly His Lys Val Pro Gln Phe
                80                      85              90

His Gly Lys Trp Pro Phe Ser Arg Phe Leu Phe Phe Gln Glu Pro
                95                     100             105

Ala Ser Ala Val Ala Ser Phe Leu Asn Gly Leu Ala Ser Leu Val
               110                     115             120

Met Leu Cys Arg Tyr Arg Thr Phe Val Pro Ala Ser Ser Pro Met
               125                     130             135

Tyr His Thr Cys Val Ala Phe Ala Trp Val Ser Leu Asn Ala Trp
               140                     145             150

Phe Trp Ser Thr Val Phe His Thr Arg Asp Thr Asp Leu Thr Glu
               155                     160             165

Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile Leu His Ser Ile
               170                     175             180

Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His Pro Ala Val
               185                     190             195

Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr Val His
               200                     205             210

Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn Leu
               215                     220             225

Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu
               230                     235             240

Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys
               245                     250             255

Cys Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu
               260                     265             270

Leu Leu Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala
               275                     280             285

Ile Trp His Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser
               290                     295             300

Phe Leu Glu Asp Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp
               305                     310             315

Lys Phe Lys Leu Asp
               320
```

<210> 300
<211> 1674
<212> DNA
<213> Homo sapiens

<400> 300
ggccgcctgg aattgtggga gttgtgtctg ccactcggct gccggaggcc 50

292

gaaggtccgt gactatggct ccccagagcc tgccttcatc taggatggct 100

cctctgggca tgctgcttgg gctgctgatg gccgcctgct tcaccttctg 150

cctcagtcat cagaacctga aggagtttgc cctgaccaac ccagagaaga 200

gcagcaccaa agaaacggag agaaaagaaa ccaaagccga ggaggagctg 250

gatgccgaag tcctggaggt gttccacccg acgcatgagt ggcaggccct 300

tcagccaggg caggctgtcc ctgcaggatc ccacgtacgg ctgaatcttc 350

agactgggga aagagaggca aaactccaat atgaggacaa gttccgaaat 400

aatttgaaag gcaaaaggct ggatatcaac accaacacct acacatctca 450

ggatctcaag agtgcactgg caaaattcaa ggaggggggca gagatggaga 500

gttcaaagga agacaaggca aggcaggctg aggtaaagcg gctcttccgc 550

cccattgagg aactgaagaa agactttgat gagctgaatg ttgtcattga 600

gactgacatg cagatcatgg tacggctgat caacaagttc aatagttcca 650

gctccagttt ggaagagaag attgctgcgc tctttgatct tgaatattat 700

gtccatcaga tggacaatgc gcaggacctg ctttcctttg gtggtcttca 750

agtggtgatc aatgggctga acagcacaga gcccctcgtg aaggagtatg 800

ctgcgtttgt gctgggcgct gccttttcca gcaaccccaa ggtccaggtg 850

gaggccatcg aaggggggagc cctgcagaag ctgctggtca tcctggccac 900

ggagcagccg ctcactgcaa agaagaaggt cctgtttgca ctgtgctccc 950

tgctgcgcca cttcccctat gcccagcggc agttcctgaa gctcggggggg 1000

ctgcaggtcc tgaggaccct ggtgcaggag aagggcacgg aggtgctcgc 1050

cgtgcgcgtg gtcacactgc tctacgacct ggtcacggag aagatgttcg 1100

ccgaggagga ggctgagctg acccaggaga tgtccccaga gaagctgcag 1150

cagtatcgcc aggtacacct cctgccaggc ctgtgggaac agggctggtg 1200

cgagatcacg gcccacctcc tggcgctgcc cgagcatgat gcccgtgaga 1250

aggtgctgca gacactgggc gtcctcctga ccacctgccg ggaccgctac 1300

cgtcaggacc cccagctcgg caggacactg gccagcctgc aggctgagta 1350

ccaggtgctg gccagcctgg agctgcagga tggtgaggac gagggctact 1400

tccaggagct gctgggctct gtcaacagct tgctgaagga gctgagatga 1450

ggccccacac caggactgga ctgggatgcc gctagtgagg ctgaggggtg 1500

293

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ccagcgtggg tgggcttctc aggcaggagg acatcttggc agtgctggct 1550

tggccattaa atggaaacct gaaggccaaa aaaaaaaaaa aaaaaaaaaa 1600

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650

aaaaaaaaaa aaaaaaaaaa aaaa 1674
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<210> 301
<211> 461
<212> PRT
<213> Homo sapiens

<400> 301
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Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly
  1               5                  10                  15

Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe Cys Leu
             20                  25                  30

Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys
             35                  40                  45

Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu
             50                  55                  60

Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu
             65                  70                  75

Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His
             80                  85                  90

Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln
             95                 100                 105

Tyr Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp
            110                 115                 120

Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu
            125                 130                 135

Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp
            140                 145                 150

Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu
            155                 160                 165

Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val Val Ile Glu Thr
            170                 175                 180

Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe Asn Ser Ser
            185                 190                 195

Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp Leu Glu
            200                 205                 210

Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser Phe
            215                 220                 225
```

294

```
Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
            230                 235                 240

Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser
            245                 250                 255

Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu
            260                 265                 270

Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala
            275                 280                 285

Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe
            290                 295                 300

Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val
            305                 310                 315

Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val
            320                 325                 330

Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe
            335                 340                 345

Ala Glu Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys
            350                 355                 360

Leu Gln Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu
            365                 370                 375

Gln Gly Trp Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu
            380                 385                 390

His Asp Ala Arg Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu
            395                 400                 405

Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg
            410                 415                 420

Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val Leu Ala Ser Leu
            425                 430                 435

Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln Glu Leu Leu
            440                 445                 450

Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg
            455                 460

<210> 302
<211> 2136
<212> DNA
<213> Homo sapiens

<400> 302
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 cccccccttc cccttccccg gggtctgggg gtgacattgc accgcgcccc 100
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```
tcgtggggtc gcgttgccac cccacgcgga ctccccagct ggcgcgcccc 150

tcccatttgc ctgtcctggt caggcccccca cccccttcc cacctgacca 200

gccatggggg ctgcggtgtt tttcggctgc actttcgtcg cgttcggccc 250

ggccttcgcg ctttttcttga tcactgtggc tggggacccg cttcgcgtta 300

tcatcctggt cgcagggca tttttctggc tggtctccct gctcctggcc 350

tctgtggtct ggttcatctt ggtccatgtg accgaccggt cagatgcccg 400

gctccagtac ggcctcctga tttttggtgc tgctgtctct gtccttctac 450

aggaggtgtt ccgctttgcc tactacaagc tgcttaagaa ggcagatgaa 500

gggttagcat cgctgagtga ggacggaaga tcacccatct ccatccgcca 550

gatggcctat gtttctggtc tctccttcgg tatcatcagt ggtgtcttct 600

ctgttatcaa tattttggct gatgcacttg gccaggtgt ggttgggatc 650

catggagact caccctatta cttcctgact tcagcctttc tgacagcagc 700

cattatcctg ctccatacct tttggggagt tgtgttcttt gatgcctgtg 750

agaggagacg gtactgggct ttgggcctgg tggttgggag tcacctactg 800

acatcgggac tgacattcct gaacccctgg tatgaggcca gcctgctgcc 850

catctatgca gtcactgttt ccatggggct ctgggccttc atcacagctg 900

gagggtccct ccgaagtatt cagcgcagcc tcttgtgtaa ggactgacta 950

cctggactga tcgcctgaca gatcccacct gcctgtccac tgcccatgac 1000

tgagcccagc cccagcccgg gtccattgcc cacattctct gtctccttct 1050

cgtcggtcta ccccactacc tccagggttt tgctttgtcc ttttgtgacc 1100

gttagtctct aagctttacc aggagcagcc tgggttcagc cagtcagtga 1150

ctggtgggtt tgaatctgca cttatcccca ccacctgggg accccttgt 1200

tgtgtccagg actcccctg tgtcagtgct ctgctctcac cctgcccaag 1250

actcacctcc cttccctct gcaggccgac ggcaggagga cagtcgggtg 1300

atggtgtatt ctgccctgcg catcccaccc gaggactgag ggaacctagg 1350

ggggacccct gggcctgggg tgccctcctg atgtcctcgc cctgtatttc 1400

tccatctcca gttctggaca gtgcaggttg ccaagaaaag ggacctagtt 1450

tagccattgc cctggagatg aaattaatgg aggctcaagg atagatgagc 1500

tctgagtttc tcagtactcc ctcaagactg gacatcttgg tcttttctc 1550
```

296

aggcctgagg gggaaccatt tttggtgtga taaataccct aaactgcctt 1600

tttttctttt ttgaggtggg gggagggagg aggtatattg gaactcttct 1650

aacctccttg ggctatattt tctctcctcg agttgctcct catggctggg 1700

ctcatttcgg tccctttctc cttggtccca gaccttgggg gaaaggaagg 1750

aagtgcatgt ttgggaactg gcattactgg aactaatggt tttaacctcc 1800

ttaaccacca gcatccctcc tctccccaag gtgaagtgga gggtgctgtg 1850

gtgagctggc cactccagag ctgcagtgcc actggaggag tcagactacc 1900

atgacatcgt agggaaggag gggagatttt tttgtagttt ttaattgggg 1950

tgtgggaggg gcggggaggt tttctataaa ctgtatcatt ttctgctgag 2000

ggtggagtgt cccatccttt taatcaaggt gattgtgatt ttgactaata 2050

aaaaagaatt tgtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2136

<210> 303
<211> 247
<212> PRT
<213> Homo sapiens

<400> 303

```
Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly
  1               5                  10                  15

Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu
                20                  25                  30

Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser
                35                  40                  45

Leu Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr
                50                  55                  60

Asp Arg Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly
                65                  70                  75

Ala Ala Val Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr
                80                  85                  90

Tyr Lys Leu Leu Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser
                95                 100                 105

Glu Asp Gly Arg Ser Pro Ile Ser Ile Arg Gln Met Ala Tyr Val
               110                 115                 120

Ser Gly Leu Ser Phe Gly Ile Ile Ser Gly Val Phe Ser Val Ile
               125                 130                 135

Asn Ile Leu Ala Asp Ala Leu Gly Pro Gly Val Val Gly Ile His
```

297

```
                    140                     145                     150

      Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser Ala Phe Leu Thr Ala
                    155                     160                     165

      Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val Val Phe Phe Asp
                    170                     175                     180

      Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu Val Val Gly
                    185                     190                     195

      Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro Trp Tyr
                    200                     205                     210

      Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met Gly
                    215                     220                     225

      Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
                    230                     235                     240

      Arg Ser Leu Leu Cys Lys Asp
                    245

<210> 304
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 108, 123, 126, 154, 198, 206, 217
<223> unknown base

<400> 304
 aagctggttt aaggaagcag aggagggtta gattcgttga gtgaggacgg 50

 aagatcaacc catttccatt ccgccagatg gcctatgttt ctggtctctc 100

 ccttcggnat catcagtggt gtnttntctg ttatcaatat tttggctgat 150

 gcanttgggc caggtgtggt tgggatccat ggagactcac cctattantt 200

 cctganttca gcctttntga cagcagccat tatcctgctc 240

<210> 305
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332
<223> unknown base

<400> 305
 gaccgaccgt tcagatgccc ggttccagta cggcttcctg atttttggtg 50

 ctgctgtntc tgtccttcta caggaggtgt tccgctttgc ctantacaag 100
```

```
ctgcttaaga aggcagatga ggggttagca tngctgagtg aggacggaag 150

atcacccatt tccatccgcc agatggccta tgtttntggt ntttccttcg 200

gtatcatcag tggtgttttn tctgttatca atattttggn tgatgcantt 250

gggccaggtg tggttgggat ccatggagan tcaccctatt aattcctgaa 300

ttcagccttt ntgacagcag ccattatcct gntccatacc ttttggggag 350

ttgtgttttt tgatgcctgt gagaggag 378
```

<210> 306
<211> 655
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1, 22, 129, 133, 184
<223> unknown base

<400> 306
```
ngttggagaa gtggcgcgga cnttcatttg gggtttcggt ttccccccctt 50

tccctttccc cggggtctgg ggtgacattg cacgggcccc tcgtggggtc 100

gcgttgccac cccacgcgga ctccccagnt gngcgccct tcccatttgc 150

ctgtcctggt caggccccca ccccccttcc cacntgacca gccatggggg 200

ctgcggtgtt tttcggctgc actttcgtcg cgttcggccc ggccttcgcg 250

cttttcttga tcactgtggc tggggacccg cttcgcgtta tcatcctggt 300

cgcaggggca tttttctggc tggtctccct gctcctggcc tctgtggtct 350

ggttcatctt ggtccatgtg accgaccggt cagatgcccg gctccagtac 400

ggcctcctga tttttggtgc tgctgtctct gtccttctac aggaggtgtt 450

ccgctttgcc tactacaagc tgcttaagaa ggcagatgag gggttagcat 500

cgctgagtga ggacggaaga tcacccatct ccatccgcca gatggcctat 550

gtttctggtc tctccttcgg tatcatcagt ggtgtcttct ctgttatcaa 600

tattttggct gatgcacttg ggccaggtgt ggttgggatc catggagact 650

caccc 655
```

<210> 307
<211> 650
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
```
299
```

<222> 52, 89, 128
<223> unknown base

<400> 307
```
gtaaaagaaa gtggccggac cttcattggg gtttcggttc cccccttttcc 50

cnttccccgg ggtctggggg tgacattgca ccgcgcccnt cgtggggtcg 100

cgttgccacc ccacgcggac tccccagntg gcgcgcccct cccatttgcc 150

tgtcctggtc aggcccccac cccccttccc acctgaccag ccatgggggc 200

tgcggtgttt ttcgggctgc actttcgtcg cgttcgggcc cggccttcgc 250

gcttttcttg atcactgtgg ctggggaccc gcttcgcgtt atcatcctgg 300

tcgcaggggc atttttctgg ctggtctccc tgctcctggc ctctgtggtc 350

tggttcatct tggtccatgt gaccgaccgg tcagatgccc ggctccagta 400

cggcctcctg attttggtg ctgctgtctc tgtccttcta caggaggtgt 450

tccgctttgc ctactacaag ctgcttaaga aggcagatga ggggttagca 500

tcgctgagtg aggacggaag atcacccatc tccatccgcc agatggccta 550

tgtttctggt ctctccttcg gtatcatcag tggtgtcttc tctgttatca 600

atattttggc tgatgcactt gggccaggtg tggttgggat ccatggagac 650
```

<210> 308
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 308
```
gccccaggga gcagtgggtg gttataactc aggcccggtg cccagagccc 50

aggaggaggc agtggccagg aaggcacagg cctgagaagt ctgcggctga 100

gctgggagca aatcccccac cccctacctg ggggacaggg caagtgagac 150

ctggtgaggg tggctcagca ggcagggaag gagaggtgtc tgtgcgtcct 200

gcacccacat ctttctctgt cccctccttg ccctgtctgg aggctgctag 250

actcctatct tctgaattct atagtgcctg ggtctcagcg cagtgccgat 300

ggtggcccgt ccttgtggtt cctctctacc tggggaaata aggtgcagcg 350

gccatggcta cagcaagacc cccctggatg tgggtgctct gtgctctgat 400

cacagccttg cttctggggg tcacagagca tgttctcgcc aacaatgatg 450

tttcctgtga ccacccctct aacaccgtgc cctctgggag caaccaggac 500

ctgggagctg gggccggggga agacgcccgg tcggatgaca gcagcagccg 550
```

300

```
catcatcaat ggatccgact gcgatatgca cacccagccg tggcaggccg 600

cgctgttgct aaggcccaac cagctctact gcggggcggt gttggtgcat 650

ccacagtggc tgctcacggc cgcccactgc aggaagaaag ttttcagagt 700

ccgtctcggc cactactccc tgtcaccagt ttatgaatct gggcagcaga 750

tgttccaggg ggtcaaatcc atcccccacc ctggctactc ccaccctggc 800

cactctaacg acctcatgct catcaaactg aacagaagaa ttcgtcccac 850

taaagatgtc agacccatca acgtctcctc tcattgtccc tctgctggga 900

caaagtgctt ggtgtctggc tggggggacaa ccaagagccc ccaagtgcac 950

ttccctaagg tcctccagtg cttgaatatc agcgtgctaa gtcagaaaag 1000

gtgcgaggat gcttacccga gacagataga tgacaccatg ttctgcgccg 1050

gtgacaaagc aggtagagac tcctgccagg gtgattctgg ggggcctgtg 1100

gtctgcaatg gctccctgca gggactcgtg tcctggggag attacccttg 1150

tgcccggccc aacagaccgg gtgtctacac gaacctctgc aagttcacca 1200

agtggatcca ggaaaccatc caggccaact cctgagtcat cccaggactc 1250

agcacaccgg catccccacc tgctgcaggg acagccctga cactccttc 1300

agaccctcat tccttcccag agatgttgag aatgttcatc tctccagccc 1350

ctgaccccat gtctcctgga ctcagggtct gcttccccca cattgggctg 1400

accgtgtctc tctagttgaa ccctgggaac aatttccaaa actgtccagg 1450

gcggggggttg cgtctcaatc tccctggggc actttcatcc tcaagctcag 1500

ggcccatccc ttctctgcag ctctgaccca aatttagtcc cagaaataaa 1550

ctgagaagtg gaaaaaaaaa 1570
```

<210> 309
<211> 293
<212> PRT
<213> Homo sapiens

<400> 309

```
Met Ala Thr Ala Arg Pro Pro Trp Met Trp Val Leu Cys Ala Leu
 1               5                  10                      15

Ile Thr Ala Leu Leu Leu Gly Val Thr Glu His Val Leu Ala Asn
               20                  25                      30

Asn Asp Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly
               35                  40                      45

Ser Asn Gln Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser
```

301

```
                    50                      55                      60
    Asp Asp Ser Ser Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met
                    65                      70                      75

    His Thr Gln Pro Trp Gln Ala Ala Leu Leu Leu Arg Pro Asn Gln
                    80                      85                      90

    Leu Tyr Cys Gly Ala Val Leu Val His Pro Gln Trp Leu Leu Thr
                    95                      100                     105

    Ala Ala His Cys Arg Lys Lys Val Phe Arg Val Arg Leu Gly His
                    110                     115                     120

    Tyr Ser Leu Ser Pro Val Tyr Glu Ser Gly Gln Gln Met Phe Gln
                    125                     130                     135

    Gly Val Lys Ser Ile Pro His Pro Gly Tyr Ser His Pro Gly His
                    140                     145                     150

    Ser Asn Asp Leu Met Leu Ile Lys Leu Asn Arg Arg Ile Arg Pro
                    155                     160                     165

    Thr Lys Asp Val Arg Pro Ile Asn Val Ser Ser His Cys Pro Ser
                    170                     175                     180

    Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr Thr Lys Ser
                    185                     190                     195

    Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn Ile Ser
                    200                     205                     210

    Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln Ile
                    215                     220                     225

    Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser
                    230                     235                     240

    Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu
                    245                     250                     255

    Gln Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn
                    260                     265                     270

    Arg Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile
                    275                     280                     285

    Gln Glu Thr Ile Gln Ala Asn Ser
                    290
```

<210> 310
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 310
 tcctgtgacc acccctctaa cacc 24

<210> 311
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 311
 ctggaacatc tgctgcccag attc 24

<210> 312
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
 gtcggatgac agcagcagcc gcatcatcaa tggatccgac tgcgatatgc 50

<210> 313
<211> 3010
<212> DNA
<213> Homo sapiens

<400> 313
 atggtcaacg accggtggaa gaccatgggc ggcgctgccc aacttgagga 50

 ccggccgcgc gacaagccgc agcggccgag ctgcggctac gtgctgtgca 100

 ccgtgctgct ggccctggct gtgctgctgg ctgtagctgt caccggtgcc 150

 gtgctcttcc tgaaccacgc ccacgcgccg ggcacggcgc ccccacctgt 200

 cgtcagcact ggggctgcca gcgccaacag cgccctggtc actgtggaaa 250

 gggcggacag ctcgcacctc agcatcctca ttgacccgcg ctgccccgac 300

 ctcaccgaca gcttcgcacg cctggagagc gcccaggcct cggtgctgca 350

 ggcgctgaca gagcaccagg cccagccacg gctggtgggc gaccaggagc 400

 aggagctgct ggacacgctg gccgaccagc tgccccggct gctggcccga 450

 gcctcagagc tgcagacgga gtgcatgggg ctgcggaagg ggcatggcac 500

 gctgggccag ggcctcagcg ccctgcagag tgagcagggc cgcctcatcc 550

 agcttctctc tgagagccag ggccacatgg ctcacctggt gaactccgtc 600

 agcgacatcc tggatgccct gcagagggac cgggggctgg gccggccccg 650

 caacaaggcc gaccttcaga gagcgcctgc ccggggaacc cggccccggg 700

303

gctgtgccac tggctcccgg ccccgagact gtctggacgt cctcctaagc 750

ggacagcagg acgatggcgt ctactctgtc tttcccaccc actacccggc 800

cggcttccag gtgtactgtg acatgcgcac ggacggcggc ggctggacgg 850

tgtttcagcg ccgggaggac ggctccgtga acttcttccg gggctgggac 900

gcgtaccgag acggctttgg caggctcacc ggggagcact ggctagggct 950

caagaggatc cacgccctga ccacacaggc tgcctacgag ctgcacgtgg 1000

acctggagga ctttgagaat ggcacggcct atgcccgcta cgggagcttc 1050

ggcgtgggct tgttctccgt ggaccctgag gaagacgggt acccgctcac 1100

cgtggctgac tattccggca ctgcaggcga ctccctcctg aagcacagcg 1150

gcatgaggtt caccaccaag gaccgtgaca gcgaccattc agagaacaac 1200

tgtgccgcct tctaccgcgg tgcctggtgg taccgcaact gccacacgtc 1250

caacctcaat gggcagtacc tgcgcggtgc gcacgcctcc tatgccgacg 1300

gcgtggagtg gtcctcctgg accggctggc agtactcact caagttctct 1350

gagatgaaga tccggccggt ccgggaggac cgctagactg gtgcaccttg 1400

tccttggccc tgctggtccc tgtcgcccca tccccgaccc cacctcactc 1450

tttcgtgaat gttctccacc cacctgtgcc tggcggaccc actctccagt 1500

agggaggggc cgggccatcc ctgacacgaa gctccctggg ccggtgaagt 1550

cacacatcgc cttctcgccg tccccacccc ctccatttgg cagctcactg 1600

atctcttgcc tctgctgatg ggggctggca aacttgacga ccccaactcc 1650

tgcctgcccc cactgtgact ccggtgctgt ttgccgtccc ctggccagga 1700

tggtggagtc tgccccaggc accctctgcc ctgcccggcc aaatacccgg 1750

cattatgggg acagagagca gggggcagac agcacccctg gagtcctcct 1800

agcagatcgt ggggaatgtc aggtctctct gaggtcaggt ctgaggccag 1850

tatcctccag ccctcccaat gccaaccccc accccgtttc cctggtgccc 1900

agagaaccca cctctcccc aagggcctca gcctggctgt gggctgggtg 1950

gccccatcct accaggccct gaggtcagga tggggagctg ctgcctttgg 2000

ggacccacgc tccaaggctg agaccagttc cctggaggcc acccaccctg 2050

tgccccggca ggcctggggt ctgcagtcct cttacctgct gtgcccacct 2100

gctctctgtc tcaaatgagg cccaacccat cccccaccca gctcccggcc 2150

304

```
gtcctcctac ctggggcagc cggggctgcc atcccatttc tcctgcctct 2200

ggaaggtggg tggggccctg caccgtgggg ctggactgcg ctaatgggaa 2250

gctcttggtt ttctgggctg gggcctaggc agggctggga tgaggcttgt 2300

acaacccca ccaccaattt cccagggact ccagggtcct gaggcctccc 2350

aggagggcct tgggggtgat gacccttcc ctgaggtggc tgtctccatg 2400

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ccggcccggc gagtggtcaa gggacaggga ccacctcacc gggcaaatgg 2500

ggtcggggg actggggcac cagaccaggc accacctgga cactttcttg 2550

ttgaatcctc ccaacaccca gcacgctgtc atccccactc cttgtgtgca 2600

cacatgcaga ggtgagaccc gcaggctccc aggaccagca gccacaaggg 2650

cagggctgga gccgggtcct cagctgtctg ctcagcagcc ctggacccgc 2700

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tggggggcctc cgaaagggct ggagtcagcc ttggggagct gcctagcagc 2800

ctctcctcgg gcaggagggg aggtggcttc ctccaaagga cacccgatgg 2850

caggtgccta gggggtgtgg ggttccgttc tcccttcccc tcccactgaa 2900

gtttgtgctt aaaaaacaat aaatttgact tggcaccact gggggttggt 2950

gggagaggcc gtgtgacctg gctctctgtc ccagtgccac caggtcatcc 3000

acatgcgcag 3010
```

<210> 314
<211> 461
<212> PRT
<213> Homo sapiens

<400> 314
```
Met Val Asn Asp Arg Trp Lys Thr Met Gly Gly Ala Ala Gln Leu
 1               5                   10                  15

Glu Asp Arg Pro Arg Asp Lys Pro Gln Arg Pro Ser Cys Gly Tyr
                20                  25                  30

Val Leu Cys Thr Val Leu Leu Ala Leu Ala Val Leu Leu Ala Val
                35                  40                  45

Ala Val Thr Gly Ala Val Leu Phe Leu Asn His Ala His Ala Pro
                50                  55                  60

Gly Thr Ala Pro Pro Pro Val Val Ser Thr Gly Ala Ala Ser Ala
                65                  70                  75

Asn Ser Ala Leu Val Thr Val Glu Arg Ala Asp Ser Ser His Leu
```

305

```
                 80                    85                    90

Ser Ile Leu Ile Asp Pro Arg Cys Pro Asp Leu Thr Asp Ser Phe
                 95                   100                   105

Ala Arg Leu Glu Ser Ala Gln Ala Ser Val Leu Gln Ala Leu Thr
                110                   115                   120

Glu His Gln Ala Gln Pro Arg Leu Val Gly Asp Gln Glu Gln Glu
                125                   130                   135

Leu Leu Asp Thr Leu Ala Asp Gln Leu Pro Arg Leu Leu Ala Arg
                140                   145                   150

Ala Ser Glu Leu Gln Thr Glu Cys Met Gly Leu Arg Lys Gly His
                155                   160                   165

Gly Thr Leu Gly Gln Gly Leu Ser Ala Leu Gln Ser Glu Gln Gly
                170                   175                   180

Arg Leu Ile Gln Leu Leu Ser Glu Ser Gln Gly His Met Ala His
                185                   190                   195

Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln Arg Asp
                200                   205                   210

Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg Ala
                215                   220                   225

Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg
                230                   235                   240

Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp
                245                   250                   255

Gly Val Tyr Ser Val Phe Pro Thr His Tyr Pro Ala Gly Phe Gln
                260                   265                   270

Val Tyr Cys Asp Met Arg Thr Asp Gly Gly Gly Trp Thr Val Phe
                275                   280                   285

Gln Arg Arg Glu Asp Gly Ser Val Asn Phe Phe Arg Gly Trp Asp
                290                   295                   300

Ala Tyr Arg Asp Gly Phe Gly Arg Leu Thr Gly Glu His Trp Leu
                305                   310                   315

Gly Leu Lys Arg Ile His Ala Leu Thr Thr Gln Ala Ala Tyr Glu
                320                   325                   330

Leu His Val Asp Leu Glu Asp Phe Glu Asn Gly Thr Ala Tyr Ala
                335                   340                   345

Arg Tyr Gly Ser Phe Gly Val Gly Leu Phe Ser Val Asp Pro Glu
                350                   355                   360

Glu Asp Gly Tyr Pro Leu Thr Val Ala Asp Tyr Ser Gly Thr Ala
                365                   370                   375
```

306

```
Gly Asp Ser Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys
              380                   385                   390

Asp Arg Asp Ser Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr
              395                   400                   405

Arg Gly Ala Trp Trp Tyr Arg Asn Cys His Thr Ser Asn Leu Asn
              410                   415                   420

Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val
              425                   430                   435

Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser
              440                   445                   450

Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg
              455                   460
```

<210> 315
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 315
 cacacgtcca acctcaatgg gcag 24

<210> 316
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 316
 gaccagcagg gccaaggaca agg 23

<210> 317
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 317
 gttctctgag atgaagatcc ggccggtccg ggagtaccgc ttag 44

<210> 318
<211> 1841
<212> DNA
<213> Homo sapiens

<400> 318
 gcagtcagag acttcccctg cccctcgctg ggaaagaaca ttaggaatgc 50

307

```
cttttagtgc cttgcttcct gaactagctc acagtagccc ggcggcccag 100

ggcaatccga ccacatttca ctctcaccgc tgtaggaatc cagatgcagg 150

ccaagtacag cagcacgagg gacatgctgg atgatgatgg ggacaccacc 200

atgagcctgc attctcaagc ctctgccaca actcggcatc cagagccccg 250

gcgcacagag cacagggctc cctcttcaac gtggcgacca gtggccctga 300

ccctgctgac tttgtgcttg gtgctgctga tagggctggc agccctgggg 350

cttttgtttt ttcagtacta ccagctctcc aatactggtc aagacaccat 400

ttctcaaatg gaagaaagat taggaaatac gtcccaagag ttgcaatctc 450

ttcaagtcca gaatataaag cttgcaggaa gtctgcagca tgtggctgaa 500

aaactctgtc gtgagctgta taacaaagct ggagcacaca ggtgcagccc 550

ttgtacagaa caatggaaat ggcatggaga caattgctac cagttctata 600

aagacagcaa aagttgggag gactgtaaat atttctgcct tagtgaaaac 650

tctaccatgc tgaagataaa caaacaagaa gacctggaat ttgccgcgtc 700

tcagagctac tctgagtttt tctactctta ttggacaggg cttttgcgcc 750

ctgacagtgg caaggcctgg ctgtggatgg atggaacccc tttcacttct 800

gaactgttcc atattataat agatgtcacc agcccaagaa gcagagactg 850

tgtggccatc ctcaatggga tgatcttctc aaaggactgc aaagaattga 900

agcgttgtgt ctgtgagaga agggcaggaa tggtgaagcc agagagcctc 950

catgtccccc ctgaaacatt aggcgaaggt gactgattcg ccctctgcaa 1000

ctacaaatag cagagtgagc caggcggtgc caaagcaagg gctagttgag 1050

acattgggaa atggaacata atcaggaaag actatctctc tgactagtac 1100

aaaatgggtt ctcgtgtttc ctgttcagga tcaccagcat ttctgagctt 1150

gggtttatgc acgtatttaa cagtcacaag aagtcttatt tacatgccac 1200

caaccaacct cagaaaccca taatgtcatc tgccttcttg gcttagagat 1250

aacttttagc tctctttctt ctcaatgtct aatatcacct ccctgttttc 1300

atgtcttcct tacacttggt ggaataagaa acttttgaa gtagaggaaa 1350

tacattgagg taacatcctt ttctctgaca gtcaagtagt ccatcagaaa 1400

ttggcagtca cttcccagat tgtaccagca aatacacaag gaattctttt 1450

tgtttgtttc agttcatact agtcccttcc caatccatca gtaaagaccc 1500
```

308

catctgcctt gtccatgccg tttcccaaca gggatgtcac ttgatatgag 1550

aatctcaaat ctcaatgcct tataagcatt ccttcctgtg tccattaaga 1600

ctctgataat tgtctccct ccataggaat ttctcccagg aaagaaatat 1650

atccccatct ccgtttcata tcagaactac cgtccccgat attcccttca 1700

gagagattaa agaccagaaa aaagtgagcc tcttcatctg cacctgtaat 1750

agtttcagtt cctattttct tccattgacc catatttata cctttcaggt 1800

actgaagatt taataataat aaatgtaaat actgtgaaaa a 1841

<210> 319
<211> 280
<212> PRT
<213> Homo sapiens

<400> 319

```
Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp
 1               5                  10                  15

Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr
            20                  25                  30

Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser
            35                  40                  45

Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val
            50                  55                  60

Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr
            65                  70                  75

Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu
            80                  85                  90

Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val
            95                  100                 105

Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys
            110                 115                 120

Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser
            125                 130                 135

Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln
            140                 145                 150

Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
            155                 160                 165

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp
            170                 175                 180

Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser
            185                 190                 195
```

309

```
Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu
             200                 205                 210

Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile
             215                 220                 225

Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
             230                 235                 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys
             245                 250                 255

Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His
             260                 265                 270

Val Pro Pro Glu Thr Leu Gly Glu Gly Asp
             275                 280
```

<210> 320
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 59, 95, 149, 331, 364, 438, 446
<223> unknown base

<400> 320
```
aattttcacc gctgtaggaa tccagatgca ggccaagtac agcagcacga 50

gggacatgnt ggatgatgat gggacaccac catgagcctg cattntcaag 100

cttttgccac aattcggcat ccagagcccc ggcgcacaga gcacagggnt 150

cctttttcaa cgtggcgacc agtggccctg accctgctga ctttgtgctt 200

ggtgctgctg atagggctgg cagccctggg gcttttgttt tttcagtact 250

accagctctc caatactggt caagacacca tttctcaaat ggaagaaaga 300

ttaggaaata cgtcccaaga gttgcaattt nttcaagtcc agaatataaa 350

gcttgcagga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400

ataacaaagc tggaggaact ttgaaggagg gcaaagtntc ctcatntact 450

atacacacac cacttccc 468
```

<210> 321
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 321

310

atgcaggcca agtacagcag cac 23

<210> 322
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 322
catgctgacg acttcctgca agc 23

<210> 323
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 323
ccacacagtc tctgcttctt ggg 23

<210> 324
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 324
atgctggatg atgatgggga caccaccatg agcctgcatt 40

<210> 325
<211> 2988
<212> DNA
<213> Homo sapiens

<400> 325
gccgagcgca agaaccctgc gcagcccaga gcagctgctg gagggggaatc 50

gaggcgcggc tccggggatt cggctcgggc cgctggctct gctctgcggg 100

gagggagcgg gcccgcccgc ggggcccgag ccctccggat ccgcccccctc 150

cccggtcccg cccccctcgga gactcctctg gctgctctgg gggttcgccg 200

gggccgggga cccgcggtcc gggcgccatg cgggcatcgc tgctgctgtc 250

ggtgctgcgg cccgcagggc ccgtggccgt gggcatctcc ctgggcttca 300

ccctgagcct gctcagcgtc acctgggtgg aggagccgtg cggcccaggc 350

ccgccccaac ctggagactc tgagctgccg ccgcgcggca acaccaacgc 400

ggcgcgccgg cccaactcgg tgcagcccgg agcggagcgc gagaagcccg 450

311

```
gggccggcga aggcgccggg gagaattggg agccgcgcgt cttgccctac 500

caccctgcac agcccggcca ggccgccaaa aaggccgtca ggacccgcta 550

catcagcacg gagctgggca tcaggcagag gctgctggtg gcggtgctga 600

cctctcagac cacgctgccc acgctgggcg tggccgtgaa ccgcacgctg 650

gggcaccggc tggagcgtgt ggtgttcctg acgggcgcac ggggccgccg 700

ggccccacct ggcatggcag tggtgacgct gggcgaggag cgacccattg 750

gacacctgca cctggcgctg cgccacctgc tggagcagca cggcgacgac 800

tttgactggt tcttcctggt gcctgacacc acctacaccg aggcgcacgg 850

cctggcacgc ctaactggcc acctcagcct ggcctccgcc gcccacctgt 900

acctgggccg gccccaggac ttcatcggcg gagagcccac ccccggccgc 950

tactgccacg gaggctttgg ggtgctgctg tcgcgcatgc tgctgcaaca 1000

actgcgcccc cacctggaag gctgccgcaa cgacatcgtc agtgcgcgcc 1050

ctgacgagtg gctgggtcgc tgcattctcg atgccaccgg ggtgggctgc 1100

actggtgacc acgaggggt gcactatagc catctggagc tgagccctgg 1150

ggagccagtg caggaggggg accctcattt ccgaagtgcc ctgacagccc 1200

accctgtgcg tgaccctgtg cacatgtacc agctgcacaa agctttcgcc 1250

cgagctgaac tggaacgcac gtaccaggag atccaggagt tacagtggga 1300

gatccagaat accagccatc tggccgttga tggggaccgg gcagctgctt 1350

ggcccgtggg tattccagca ccatcccgcc cggcctcccg ctttgaggtg 1400

ctgcgctggg actacttcac ggagcagcac gctttctcct gcgccgatgg 1450

ctcaccccgc tgcccactgc gtggggctga ccgggctgat gtggccgatg 1500

ttctggggac agctctagag gagctgaacc gccgctacca cccggccttg 1550

cggctccaga agcagcagct ggtgaatggc taccgacgct ttgatccggc 1600

ccggggtatg gaatacacgc tggacttgca gctggaggca ctgaccccc 1650

agggaggccg ccggcccctc actcgccgag tgcagctgct ccggccgctg 1700

agccgcgtgg agatcttgcc tgtgccctat gtcactgagg cctcacgtct 1750

cactgtgctg ctgcctctag ctgcggctga gcgtgacctg gccctggct 1800

tcttggaggc ctttgccact gcagcactgg agcctggtga tgctgcggca 1850

gccctgaccc tgctgctact gtatgagccg cgccaggccc agcgcgtggc 1900
```

312

```
ccatgcagat gtcttcgcac ctgtcaaggc ccacgtggca gagctggagc 1950

ggcgtttccc cggtgcccgg gtgccatggc tcagtgtgca gacagccgca 2000

ccctcaccac tgcgcctcat ggatctactc tccaagaagc acccgctgga 2050

cacactgttc ctgctggccg ggccagacac ggtgctcacg cctgacttcc 2100

tgaaccgctg ccgcatgcat gccatctccg gctggcaggc cttctttccc 2150

atgcatttcc aagccttcca cccaggtgtg gccccaccac aagggcctgg 2200

gcccccagag ctgggccgtg acactggccg ctttgatcgc caggcagcca 2250

gcgaggcctg cttctacaac tccgactacg tggcagcccg tgggcgcctg 2300

gcggcagcct cagaacaaga agaggagctg ctggagagcc tggatgtgta 2350

cgagctgttc ctccacttct ccagtctgca tgtgctgcgg cggtggagc 2400

cggcgctgct gcagcgctac cgggcccaga cgtgcagcgc gaggctcagt 2450

gaggacctgt accaccgctg cctccagagc gtgcttgagg gcctcggctc 2500

ccgaacccag ctggccatgc tactctttga acaggagcag ggcaacagca 2550

cctgacccca ccctgtcccc gtgggccgtg gcatggccac accccacccc 2600

acttctcccc caaaaccaga gccacctgcc agcctcgctg ggcagggctg 2650

gccgtagcca daccccaagc tggcccactg gtccctctc tggctctgtg 2700

ggtccctggg ctctggacaa gcactggggg acgtgccccc agagccaccc 2750

acttctcatc ccaaacccag tttccctgcc ccctgacgct gctgattcgg 2800

gctgtggcct ccacgtattt atgcagtaca gtctgcctga cgccagccct 2850

gcctctgggc cctgggggct gggctgtaga agagttgttg gggaaggagg 2900

gagctgagga gggggcatct cccaacttct cccttttgga ccctgccgaa 2950

gctccctgcc tttaataaac tggccaagtg tggaaaaa 2988
```

```
<210> 326
<211> 775
<212> PRT
<213> Homo sapiens

<400> 326
Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro
  1               5                  10                  15

Val Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser
               20                  25                  30

Val Thr Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro
               35                  40                  45
```

313

```
Gly Asp Ser Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg
                50                  55                  60

Arg Pro Asn Ser Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly
                65                  70                  75

Ala Gly Glu Gly Ala Gly Glu Asn Trp Glu Pro Arg Val Leu Pro
                80                  85                  90

Tyr His Pro Ala Gln Pro Gly Gln Ala Ala Lys Lys Ala Val Arg
                95                  100                 105

Thr Arg Tyr Ile Ser Thr Glu Leu Gly Ile Arg Gln Arg Leu Leu
                110                 115                 120

Val Ala Val Leu Thr Ser Gln Thr Thr Leu Pro Thr Leu Gly Val
                125                 130                 135

Ala Val Asn Arg Thr Leu Gly His Arg Leu Glu Arg Val Val Phe
                140                 145                 150

Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro Pro Gly Met Ala Val
                155                 160                 165

Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His Leu His Leu Ala
                170                 175                 180

Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe Asp Trp Phe
                185                 190                 195

Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly Leu Ala
                200                 205                 210

Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu Tyr
                215                 220                 225

Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly
                230                 235                 240

Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu
                245                 250                 255

Leu Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile
                260                 265                 270

Val Ser Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp
                275                 280                 285

Ala Thr Gly Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr
                290                 295                 300

Ser His Leu Glu Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp
                305                 310                 315

Pro His Phe Arg Ser Ala Leu Thr Ala His Pro Val Arg Asp Pro
                320                 325                 330

Val His Met Tyr Gln Leu His Lys Ala Phe Ala Arg Ala Glu Leu
```

314

```
                335                    340                    345
Glu Arg Thr Tyr Gln Glu Ile Gln Glu Leu Gln Trp Glu Ile Gln
                350                    355                    360
Asn Thr Ser His Leu Ala Val Asp Gly Asp Arg Ala Ala Ala Trp
                365                    370                    375
Pro Val Gly Ile Pro Ala Pro Ser Arg Pro Ala Ser Arg Phe Glu
                380                    385                    390
Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln His Ala Phe Ser Cys
                395                    400                    405
Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly Ala Asp Arg Ala
                410                    415                    420
Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu Leu Asn Arg
                425                    430                    435
Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu Val Asn
                440                    445                    450
Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu
                455                    460                    465
Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro
                470                    475                    480
Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu
                485                    490                    495
Ile Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val
                500                    505                    510
Leu Leu Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe
                515                    520                    525
Leu Glu Ala Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala
                530                    535                    540
Ala Ala Leu Thr Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln
                545                    550                    555
Arg Val Ala His Ala Asp Val Phe Ala Pro Val Lys Ala His Val
                560                    565                    570
Ala Glu Leu Glu Arg Arg Phe Pro Gly Ala Arg Val Pro Trp Leu
                575                    580                    585
Ser Val Gln Thr Ala Ala Pro Ser Pro Leu Arg Leu Met Asp Leu
                590                    595                    600
Leu Ser Lys Lys His Pro Leu Asp Thr Leu Phe Leu Leu Ala Gly
                605                    610                    615
Pro Asp Thr Val Leu Thr Pro Asp Phe Leu Asn Arg Cys Arg Met
                620                    625                    630
```

315

```
His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro Met His Phe Gln
                635                 640                 645

Ala Phe His Pro Gly Val Ala Pro Pro Gln Gly Pro Gly Pro Pro
                650                 655                 660

Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln Ala Ala Ser
                665                 670                 675

Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly Arg
                680                 685                 690

Leu Ala Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser Leu
                695                 700                 705

Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu
                710                 715                 720

Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr
                725                 730                 735

Cys Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln
                740                 745                 750

Ser Val Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu
                755                 760                 765

Leu Phe Glu Gln Glu Gln Gly Asn Ser Thr
                770                 775
```

<210> 327
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
 tggaaggctg ccgcaacgac aatc 24

<210> 328
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
 ctgatgtggc cgatgttctg 20

<210> 329
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 329
 atggctcagt gtgcagacag 20

<210> 330
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 330
 gcatgctgct ccgtgaagta gtcc 24

<210> 331
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 331
 atgcatggga aagaaggcct gccc 24

<210> 332
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 332
 tgcactggtg accacgaggg ggtgcactat agccatctgg agctgag 47

<210> 333
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 333
 gctctggccg gccccggcga ttggtcaccg cccgctaggg gacagccctg 50

 gcctcctctg attggcaagc gctggccacc tccccacacc ccttgcgaac 100

 gctcccctag tggagaaaag gagtagctat tagccaattc ggcagggccc 150

 gctttttaga agcttgattt cctttgaaga tgaaagacta gcggaagctc 200

 tgcctctttc cccagtgggc gagggaactc ggggcgattg gctgggaact 250

 gtatccaccc aaatgtcacc gatttcttcc tatgcaggaa atgagcagac 300

 ccatcaataa gaaatttctc agcctggccg aaaatggttg gccccacgaa 350

317

```
Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala
 1               5                  10                  15

Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu
                20                  25                  30

Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly
                35                  40                  45

Lys Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu
                50                  55                  60

Pro Glu Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly
                65                  70                  75

Tyr Asp Lys Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val
                80                  85                  90

Phe Phe Phe Gly Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe
                95                  100                 105

Val Ala Tyr Leu Pro Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg
```

318

```
                 110                  115                  120
```

```
  Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro
                  125                  130                  135

  Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro
                  140                  145                  150

  Glu Asp Glu
```

<210> 335
<211> 442
<212> DNA
<213> Homo sapiens

<400> 335

```
 ggcggctggg ctgtttggtt tgagcgctcg ccgtcttttg gcggcagcgg 50

 cgacgcgagg gctcccggcc gcccgcgtcc gctgggaatc tagcttctcc 100

 aggactgtgg tcgccccgtc cgctgtggcg ggaaagcggc ccccagaacc 150

 gaccacaccg tggcaagagg acccagaacc cgaggacgaa aacttgtatg 200

 agaagaaccc agactcccat ggttatgaca aggaccccgt tttggacgtc 250

 tggaacatgc gacttgtctt cttctttggc gtctccatca tcctggtcct 300

 tggcagcacc tttgtggcct atctgcctga ctacaggatg aaagagtggt 350

 cccgccgcga agctgagagg cttgtgaaat accgagaggc caatggcctt 400

 cccatcatgg aatccaactg cttcgacccc agcaagatcc ag 442
```

<210> 336
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 336
 ctgagaccct gcagcaccat ctg 23

<210> 337
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 337
 ggtgcttctt gagccccact tagc 24

<210> 338

319

<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 338
 aatctagctt ctccaggact gtggtcgccc cgtccgctgt 40

<210> 339
<211> 2162
<212> DNA
<213> Homo sapiens

<400> 339
 gcggcggcta tgccgcttgc tctgctcgtc ctgttgctcc tggggcccgg 50

 cggctggtgc cttgcagaac ccccacgcga cagcctgcgg gaggaacttg 100

 tcatcacccc gctgccttcc ggggacgtag ccgccacatt ccagttccgc 150

 acgcgctggg attcggagct tcagcgggaa ggagtgtccc attacaggct 200

 ctttcccaaa gccctggggc agctgatctc caagtattct ctacgggagc 250

 tgcacctgtc attcacacaa ggcttttgga ggacccgata ctgggggcca 300

 cccttcctgc aggccccatc aggtgcagag ctgtgggtct ggttccaaga 350

 cactgtcact gatgtggata aatcttggaa ggagctcagt aatgtcctct 400

 cagggatctt ctgcgcctct ctcaacttca tcgactccac caacacagtc 450

 actcccactg cctccttcaa acccctgggt ctggccaatg acactgacca 500

 ctactttctg cgctatgctg tgctgccgcg ggaggtggtc tgcaccgaaa 550

 acctcacccc ctggaagaag ctcttgccct gtagttccaa ggcaggcctc 600

 tctgtgctgc tgaaggcaga tcgcttgttc cacaccagct accactccca 650

 ggcagtgcat atccgccctg tttgcagaaa tgcacgctgt actagcatct 700

 cctgggagct gaggcagacc ctgtcagttg tatttgatgc cttcatcacg 750

 gggcagggaa agaaagactg gtccctcttc cggatgttct cccgaaccct 800

 cacggagccc tgccccctgg cttcagagag ccgagtctat gtggacatca 850

 ccacctacaa ccaggacaac gagacattag aggtgcaccc acccccgacc 900

 actacatatc aggacgtcat cctaggcact cggaagacct atgccatcta 950

 tgacttgctt gacaccgcca tgatcaacaa ctctcgaaac ctcaacatcc 1000

 agctcaagtg gaagagaccc ccagagaatg aggccccccc agtgcccttc 1050

320

ctgcatgccc agcggtacgt gagtggctat gggctgcaga agggggagct 1100

gagcacactg ctgtacaaca cccacccata ccgggccttc ccggtgctgc 1150

tgctggacac cgtaccctgg tatctgcggc tgtatgtgca caccctcacc 1200

atcacctcca agggcaagga gaacaaacca agttacatcc actaccagcc 1250

tgcccaggac cggctgcaac cccacctcct ggagatgctg attcagctgc 1300

cggccaactc agtcaccaag gtttccatcc agtttgagcg ggcgctgctg 1350

aagtggaccg agtacacgcc agatcctaac catggcttct atgtcagccc 1400

atctgtcctc agcgcccttg tgcccagcat ggtagcagcc aagccagtgg 1450

actgggaaga gagtcccctc ttcaacagcc tgttcccagt ctctgatggc 1500

tctaactact ttgtgcggct ctacacggag ccgctgctgg tgaacctgcc 1550

gacaccggac ttcagcatgc cctacaacgt gatctgcctc acgtgcactg 1600

tggtggccgt gtgctacggc tccttctaca atctcctcac ccgaaccttc 1650

cacatcgagg agccccgcac aggtggcctg gccaagcggc tggccaacct 1700

tatccggcgc gcccgaggtg tcccccccact ctgattcttg cccttttccag 1750

cagctgcagc tgccgtttct ctctggggag gggagcccaa gggctgtttc 1800

tgccacttgc tctcctcaga gttggctttt gaaccaaagt gccctggacc 1850

aggtcagggc ctacagctgt gttgtccagt acaggagcca cgagccaaat 1900

gtggcatttg aatttgaatt aacttagaaa ttcatttcct cacctgtagt 1950

ggccacctct atattgaggt gctcaataag caaaagtggt cggtggctgc 2000

tgtattggac agcacagaaa aagatttcca tcaccacaga aaggtcggct 2050

ggcagcactg gccaaggtga tggggtgtgc tacacagtgt atgtcactgt 2100

gtagtggatg gagtttactg tttgtggaat aaaaacggct gtttccgtgg 2150

aaaaaaaaaa aa 2162

<210> 340
<211> 574
<212> PRT
<213> Homo sapiens

<400> 340
Met Pro Leu Ala Leu Leu Val Leu Leu Leu Gly Pro Gly Gly
  1   5   10   15

Trp Cys Leu Ala Glu Pro Pro Arg Asp Ser Leu Arg Glu Glu Leu
                  20   25   30

Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala Thr Phe Gln
          35   40   45

Phe Arg Thr Arg Trp Asp Ser Glu Leu Gln Arg Glu Gly Val Ser
          50   55   60

His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser Lys
          65   70   75

Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
          80   85   90

Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly
          95   100   105

Ala Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp
          110   115   120

Lys Ser Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys
          125   130   135

Ala Ser Leu Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr
          140   145   150

Ala Ser Phe Lys Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr
          155   160   165

Phe Leu Arg Tyr Ala Val Leu Pro Arg Glu Val Val Cys Thr Glu
          170   175   180

Asn Leu Thr Pro Trp Lys Lys Leu Leu Pro Cys Ser Ser Lys Ala
          185   190   195

Gly Leu Ser Val Leu Leu Lys Ala Asp Arg Leu Phe His Thr Ser
          200   205   210

Tyr His Ser Gln Ala Val His Ile Arg Pro Val Cys Arg Asn Ala
          215   220   225

Arg Cys Thr Ser Ile Ser Trp Glu Leu Arg Gln Thr Leu Ser Val
          230   235   240

Val Phe Asp Ala Phe Ile Thr Gly Gln Gly Lys Lys Asp Trp Ser
          245   250   255

Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu Pro Cys Pro Leu
          260   265   270

Ala Ser Glu Ser Arg Val Tyr Val Asp Ile Thr Thr Tyr Asn Gln
          275   280   285

Asp Asn Glu Thr Leu Glu Val His Pro Pro Pro Thr Thr Thr Tyr
          290   295   300

Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Ile Tyr Asp
          305   310   315

Leu Leu Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile

322

```
                 320                      325                      330
    Gln Leu Lys Trp Lys Arg Pro Pro Glu Asn Glu Ala Pro Pro Val
                     335                 340                 345

    Pro Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln
                     350                 355                 360

    Lys Gly Glu Leu Ser Thr Leu Leu Tyr Asn Thr His Pro Tyr Arg
                     365                 370                 375

    Ala Phe Pro Val Leu Leu Leu Asp Thr Val Pro Trp Tyr Leu Arg
                     380                 385                 390

    Leu Tyr Val His Thr Leu Thr Ile Thr Ser Lys Gly Lys Glu Asn
                     395                 400                 405

    Lys Pro Ser Tyr Ile His Tyr Gln Pro Ala Gln Asp Arg Leu Gln
                     410                 415                 420

    Pro His Leu Leu Glu Met Leu Ile Gln Leu Pro Ala Asn Ser Val
                     425                 430                 435

    Thr Lys Val Ser Ile Gln Phe Glu Arg Ala Leu Leu Lys Trp Thr
                     440                 445                 450

    Glu Tyr Thr Pro Asp Pro Asn His Gly Phe Tyr Val Ser Pro Ser
                     455                 460                 465

    Val Leu Ser Ala Leu Val Pro Ser Met Val Ala Ala Lys Pro Val
                     470                 475                 480

    Asp Trp Glu Glu Ser Pro Leu Phe Asn Ser Leu Phe Pro Val Ser
                     485                 490                 495

    Asp Gly Ser Asn Tyr Phe Val Arg Leu Tyr Thr Glu Pro Leu Leu
                     500                 505                 510

    Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr Asn Val Ile
                     515                 520                 525

    Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser Phe Tyr
                     530                 535                 540

    Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Arg Thr Gly
                     545                 550                 555

    Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly
                     560                 565                 570

    Val Pro Pro Leu
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<210> 341
<211> 24
<212> DNA
<213> Artificial Sequence

323

<220>
<223> Synthetic oligonucleotide probe

<400> 341
 tggacaccgt accctggtat ctgc 24

<210> 342
<211> 24
<212> DNA
<213> Artificial Seqeunce

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic oligonucleotide probe

<400> 342
 ccaactctga ggagagcaag tggc 24

<210> 343
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 343
 tgtatgtgca caccctcacc atcacctcca agggcaagga gaac 44

<210> 344
<211> 762
<212> DNA
<213> Homo sapiens

<400> 344
 caacatgggg tccagcagct tcttggtcct catggtgtct ctcgttcttg 50

 tgaccctggt ggctgtggaa ggagttaaag agggtataga gaaagcaggg 100

 gtttgcccag ctgacaacgt acgctgcttc aagtccgatc ctccccagtg 150

 tcacacagac caggactgtc tggggaaag gaagtgttgt tacctgcact 200

 gtggcttcaa gtgtgtgatt cctgtgaagg aactggaaga aggaggaaac 250

 aaggatgaag atgtgtcaag gccataccct gagccaggat gggaggccaa 300

 gtgtccaggc tcctcctcta ccaggtgtcc tcagaaatga tgctgggtcc 350

 tttctacctc tggggtcac tctcacttgg cacctgcccc tgagggtcct 400

 gagacttgga atatggaaga agcaataccc aacccccacca aagaaaacct 450

 gagcttgaag tccttttccc caaaaagagg gaagagtcac aaaaagtcca 500

 gaccccaggg acggtacttt ccctctctac ctggtgctcc tccctaatgc 550

tcatgaatgg acccctcatg aatgaaacca gtgcccttat aagagacccc 600

aaagagctgc cttgcccttc tgcaatgtgt gatcacagct agaaggcact 650

gtcagagaag agaaactggt cctcaccaga tgctgaatct gctggtgcct 700

tgatcttgga cttcccagcc tctagaactg taagaaataa atatttgctg 750

tttataatcc aa 762

<210> 345
<211> 111
<212> PRT
<213> Homo sapiens

<400> 345

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Met Gly Ser Ser Ser Phe Leu Val Leu Met Val Ser Leu Val Leu
  1               5                  10                  15

Val Thr Leu Val Ala Val Glu Gly Val Lys Glu Gly Ile Glu Lys
             20                  25                  30

Ala Gly Val Cys Pro Ala Asp Asn Val Arg Cys Phe Lys Ser Asp
             35                  40                  45

Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys
             50                  55                  60

Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys
             65                  70                  75

Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro
             80                  85                  90

Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser
             95                 100                 105

Thr Arg Cys Pro Gln Lys
                110
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<210> 346
<211> 2528
<212> DNA
<213> Homo sapiens

<400> 346

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ttcctggcca ggaaacctga gcggtgagac tcccagctgc ctacatcaag 100

gccccaggac atgcagaacc ttcctctaga acccgacccca ccaccatgag 150

gtcctgcctg tggagatgca ggcacctgag ccaaggcgtc cagtggtcct 200

tgcttctggc tgtcctggtc ttctttctct tcgccttgcc ctctttttatt 250

aaggagcctc aaacaaagcc ttccaggcat caacgcacag agaacattaa 300

325

agaaaggtct ctacagtccc tggcaaagcc taagtcccag gcacccacaa 350

gggcgaggag acaaccatc tatgcagagc cagcgccaga gaacaatgcc 400

ctcaacacac aaacccagcc caaggcccac accaccggag acagaggaaa 450

ggaggccaac caggcaccgc cggaggagca ggacaaggtg ccccacacag 500

cacagagggc agcatggaag agcccagaaa aagagaaaac catggtgaac 550

acactgtcac ccagagggca agatgcaggg atggcctctg gcaggacaga 600

ggcacaatca tggaagagcc aggacacaaa gacgacccaa ggaaatgggg 650

gccagaccag gaagctgacg gcctccagga cggtgtcaga gaagcaccag 700

ggcaaagcgg caaccacagc caagacgctc attcccaaaa gtcagcacag 750

aatgctggct cccacaggag cagtgtcaac aaggacgaga cagaaaggag 800

tgaccacagc agtcatccca cctaaggaga agaaacctca ggccacccca 850

ccccctgccc ctttccagag ccccacgacg cagagaaacc aaagactgaa 900

ggccgccaac ttcaaatctg agcctcggtg ggattttgag gaaaaataca 950

gcttcgaaat aggaggcctt cagacgactt gccctgactc tgtgaagatc 1000

aaagcctcca agtcgctgtg gctccagaaa ctctttctgc ccaacctcac 1050

tctcttcctg gactccagac acttcaacca gagtgagtgg gaccgcctgg 1100

aacactttgc accaccctttt ggcttcatgg agctcaacta ctccttggtg 1150

cagaaggtcg tgacacgctt ccctccagtg ccccagcagc agctgctcct 1200

ggccagcctc cccgctggga gcctccggtg catcacctgt gccgtggtgg 1250

gcaacggggg catcctgaac aactcccaca tgggccagga gatagacagt 1300

cacgactacg tgttccgatt gagcggagct ctcattaaag gctacgaaca 1350

ggatgtgggg actcggacat ccttctacgg ctttaccgcc ttctccctga 1400

cccagtcact ccttatattg ggcaatcggg gtttcaagaa cgtgcctctt 1450

gggaaggacg tccgctactt gcacttcctg gaaggcaccc gggactatga 1500

gtggctggaa gcactgctta tgaatcagac ggtgatgtca aaaaccttt 1550

tctggttcag gcacagaccc caggaagctt ttcgggaagc cctgcacatg 1600

gacaggtacc tgttgctgca cccagacttt ctccgataca tgaagaacag 1650

gtttctgagg tctaagaccc tggatggtgc ccactggagg atataccgcc 1700

ccaccactgg ggccctcctg ctgctcactg cccttcagct ctgtgaccag 1750

326

gtgagtgctt atggcttcat cactgagggc catgagcgct tttctgatca 1800

ctactatgat acatcatgga agcggctgat cttttacata aaccatgact 1850

tcaagctgga gagagaagtc tggaagcggc tacacgatga agggataatc 1900

cggctgtacc agcgtcctgg tcccggaact gccaaagcca agaactgacc 1950

ggggccaggg ctgccatggt ctccttgcct gctccaaggc acaggataca 2000

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caagcccttc aggagttcca agggaacact tgaaccatgg acaagactct 2100

ctcaagatgg caaatggcta attgaggttc tgaagttctt cagtacattg 2150

ctgtaggtcc tgaggccagg gattttaat taaatggggt gatgggtggc 2200

caataccaca attcctgctg aaaaacactc ttccagtcca aaagcttctt 2250

gatacagaaa aagagcctg gatttacaga aacatataga tctggtttga 2300

attccagatc gagtttacag ttgtgaaatc ttgaaggtat tacttaactt 2350

cactacagat tgtctagaag acctttctag gagttatctg attctagaag 2400

ggtctatact tgtccttgtc tttaagctat ttgacaactc tacgtgttgt 2450

agaaaactga taataataca aatgattgtt gtccatggaa aggcaaataa 2500

attttctaca gtgaaaaaaa aaaaaaaa 2528

<210> 347
<211> 600
<212> PRT
<213> Homo sapiens

<400> 347
Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val
  1   5   10   15

Gln Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala
                 20   25   30

Leu Pro Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His
                 35   40   45

Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala
                 50   55   60

Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile
                 65   70   75

Tyr Ala Glu Pro Ala Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr
                 80   85   90

Gln Pro Lys Ala His Thr Thr Gly Asp Arg Gly Lys Glu Ala Asn
                 95   100   105

327

Gln Ala Pro Pro Glu Glu Gln Asp Lys Val Pro His Thr Ala Gln
           110   115   120

Arg Ala Ala Trp Lys Ser Pro Glu Lys Glu Lys Thr Met Val Asn
           125   130   135

Thr Leu Ser Pro Arg Gly Gln Asp Ala Gly Met Ala Ser Gly Arg
           140   145   150

Thr Glu Ala Gln Ser Trp Lys Ser Gln Asp Thr Lys Thr Thr Gln
           155   160   165

Gly Asn Gly Gly Gln Thr Arg Lys Leu Thr Ala Ser Arg Thr Val
           170   175   180

Ser Glu Lys His Gln Gly Lys Ala Ala Thr Thr Ala Lys Thr Leu
           185   190   195

Ile Pro Lys Ser Gln His Arg Met Leu Ala Pro Thr Gly Ala Val
           200   205   210

Ser Thr Arg Thr Arg Gln Lys Gly Val Thr Thr Ala Val Ile Pro
           215   220   225

Pro Lys Glu Lys Lys Pro Gln Ala Thr Pro Pro Pro Ala Pro Phe
           230   235   240

Gln Ser Pro Thr Thr Gln Arg Asn Gln Arg Leu Lys Ala Ala Asn
           245   250   255

Phe Lys Ser Glu Pro Arg Trp Asp Phe Glu Glu Lys Tyr Ser Phe
           260   265   270

Glu Ile Gly Gly Leu Gln Thr Thr Cys Pro Asp Ser Val Lys Ile
           275   280   285

Lys Ala Ser Lys Ser Leu Trp Leu Gln Lys Leu Phe Leu Pro Asn
           290   295   300

Leu Thr Leu Phe Leu Asp Ser Arg His Phe Asn Gln Ser Glu Trp
           305   310   315

Asp Arg Leu Glu His Phe Ala Pro Pro Phe Gly Phe Met Glu Leu
           320   325   330

Asn Tyr Ser Leu Val Gln Lys Val Val Thr Arg Phe Pro Pro Val
           335   340   345

Pro Gln Gln Gln Leu Leu Leu Ala Ser Leu Pro Ala Gly Ser Leu
           350   355   360

Arg Cys Ile Thr Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn
           365   370   375

Asn Ser His Met Gly Gln Glu Ile Asp Ser His Asp Tyr Val Phe
           380   385   390

Arg Leu Ser Gly Ala Leu Ile Lys Gly Tyr Glu Gln Asp Val Gly

Thr Arg Thr Ser Phe Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln
          410   415   420

Ser Leu Leu Ile Leu Gly Asn Arg Gly Phe Lys Asn Val Pro Leu
              425   430   435

Gly Lys Asp Val Arg Tyr Leu His Phe Leu Glu Gly Thr Arg Asp
              440   445   450

Tyr Glu Trp Leu Glu Ala Leu Leu Met Asn Gln Thr Val Met Ser
              455   460   465

Lys Asn Leu Phe Trp Phe Arg His Arg Pro Gln Glu Ala Phe Arg
              470   475   480

Glu Ala Leu His Met Asp Arg Tyr Leu Leu Leu His Pro Asp Phe
              485   490   495

Leu Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu Asp
              500   505   510

Gly Ala His Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu
              515   520   525

Leu Leu Thr Ala Leu Gln Leu Cys Asp Gln Val Ser Ala Tyr Gly
              530   535   540

Phe Ile Thr Glu Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp
              545   550   555

Thr Ser Trp Lys Arg Leu Ile Phe Tyr Ile Asn His Asp Phe Lys
              560   565   570

Leu Glu Arg Glu Val Trp Lys Arg Leu His Asp Glu Gly Ile Ile
              575   580   585

Arg Leu Tyr Gln Arg Pro Gly Pro Gly Thr Ala Lys Ala Lys Asn
              590   595   600

<210> 348
<211> 496
<212> DNA
<213> Homo sapiens

<400> 348
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 gggccttcgc cggagcagcg agtggaaatt gttcctcgag atctgaggat 100

 gaaggacaag tttctaaaac accttacagg ccctctttat tttagtccaa 150

 agtgcagcaa acacttccat agactttatc acaacaccag agactgcacc 200

 attcctgcat actataaaag atgcgccagg cttcttaccc ggctggctgt 250

 cagtccagtg tgcatggagg ataagtgagc agaccgtaca ggagcagcac 300

329

accaggagcc atgagaagtg ccttggaaac caacagggaa acagaactat 350

ctttatacac atcccctcat ggacaagaga tttatttttg cagacagact 400

cttccataag tcctttgagt tttgtatgtt gttgacagtt tgcagatata 450

tattcgataa atcagtgtac ttgacagtgt tatctgtcac ttattt 496

<210> 349
<211> 91
<212> PRT
<213> Homo sapiens

<400> 349
Met Arg Gly Pro Gly His Pro Leu Leu Leu Gly Leu Leu Leu Val
  1   5   10   15

Leu Gly Pro Ser Pro Glu Gln Arg Val Glu Ile Val Pro Arg Asp
               20   25   30

Leu Arg Met Lys Asp Lys Phe Leu Lys His Leu Thr Gly Pro Leu
               35   40   45

Tyr Phe Ser Pro Lys Cys Ser Lys His Phe His Arg Leu Tyr His
               50   55   60

Asn Thr Arg Asp Cys Thr Ile Pro Ala Tyr Tyr Lys Arg Cys Ala
               65   70   75

Arg Leu Leu Thr Arg Leu Ala Val Ser Pro Val Cys Met Glu Asp
               80   85   90

Lys

<210> 350
<211> 1141
<212> DNA
<213> Homo sapiens

<400> 350
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ttctctggga ggcccgaccc cggccgcgcc cagcccccac catgccaccc 100

gcggggctcc gccgggccgc gccgctcacc gcaatcgctc tgttggtgct 150

gggggctccc ctggtgctgg ccggcgagga ctgcctgtgg tacctggacc 200

ggaatggctc ctggcatccg gggtttaact gcgagttctt caccttctgc 250

tgcgggacct gctaccatcg gtactgctgc agggacctga ccttgcttat 300

caccgagagg cagcagaagc actgcctggc cttcagcccc aagaccatag 350

caggcatcgc ctcagctgtg atcctctttg ttgctgtggt tgccaccacc 400

atctgctgct cctctgttc ctgttgctac ctgtaccgcc ggcgccagca 450

330

gctccagagc ccatttgaag gccaggagat tccaatgaca ggcatcccag 500

tgcagccagt atacccatac ccccaggacc ccaaagctgg ccctgcaccc 550

ccacagcctg gcttcatgta cccacctagt ggtcctgctc cccaatatcc 600

actctaccca gctgggcccc cagtctacaa ccctgcagct cctcctccct 650

atatgccacc acagccctct tacccgggag cctgaggaac cagccatgtc 700

tctgctgccc cttcagtgat gccaaccttg ggagatgccc tcatcctgta 750

cctgcatctg gtcctggggg tggcaggagt cctccagcca ccaggcccca 800

gaccaagcca gccctgggc cctactgggg acagagcccc agggaagtgg 850

aacaggagct gaactagaac tatgaggggt tggggggagg gcttggaatt 900

atgggctatt tttactgggg gcaagggagg gagatgacag cctgggtcac 950

agtgcctgtt ttcaaatagt ccctctgctc ccaagatccc agccaggaag 1000

gctggggccc tactgtttgt cccctctggg ctggggtggg gggaggggagg 1050

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ccacatctct ggcctgctag attaaagctg taaagacaaa a 1141

<210> 351
<211> 197
<212> PRT
<213> Homo sapiens

<400> 351
Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile
1   5   10   15

Ala Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp
                20   25   30

Cys Leu Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe
                35   40   45

Asn Cys Glu Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg
                50   55   60

Tyr Cys Cys Arg Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln
                65   70   75

Lys His Cys Leu Ala Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala
                80   85   90

Ser Ala Val Ile Leu Phe Val Ala Val Val Ala Thr Thr Ile Cys
                95   100   105

Cys Phe Leu Cys Ser Cys Cys Tyr Leu Tyr Arg Arg Arg Gln Gln
                110   115   120

331

```
Leu Gln Ser Pro Phe Glu Gly Gln Glu Ile Pro Met Thr Gly Ile
            125                 130                     135

Pro Val Gln Pro Val Tyr Pro Tyr Pro Gln Asp Pro Lys Ala Gly
            140                 145                     150

Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr Pro Pro Ser Gly Pro
            155                 160                     165

Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro Pro Val Tyr Asn
            170                 175                     180

Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro
            185                 190                     195

Gly Ala
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<210> 352
<211> 3226
<212> DNA
<213> Homo sapiens

<400> 352
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 gcggccccag aaccccaggt aggtagagca agaagatggt gtttctgccc  100

 ctcaaatggt cccttgcaac catgtcattt ctactttcct cactgttggc  150

 tctcttaact gtgtccactc cttcatggtg tcagagcact gaagcatctc  200

 caaaacgtag tgatgggaca ccatttcctt ggaataaaat acgacttcct  250

 gagtacgtca tcccagttca ttatgatctc ttgatccatg caaaccttac  300

 cacgctgacc ttctggggaa ccacgaaagt agaaatcaca gccagtcagc  350

 ccaccagcac catcatcctg catagtcacc acctgcagat atctagggcc  400

 accctcagga agggagctgg agagaggcta tcggaagaac ccctgcaggt  450

 cctggaacac cccctcagg agcaaattgc actgctggct cccgagcccc  500

 tccttgtcgg gctcccgtac acagttgtca ttcactatgc tggcaatctt  550

 tcggagactt ccacggatt ttacaaaagc acctacagaa ccaaggaagg  600

 ggaactgagg atactagcat caacacaatt tgaacccact gcagctagaa  650

 tggcctttcc ctgctttgat gaacctgcct tcaaagcaag tttctcaatc  700

 aaaattagaa gagagccaag gcacctagcc atctccaata tgccattggt  750

 gaaatctgtg actgttgctg aaggactcat agaagaccat tttgatgtca  800

 ctgtgaagat gagcacctat ctggtggcct tcatcatttc agattttgag  850
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332

tctgtcagca agataaccaa gagtggagtc aaggtttctg tttatgctgt 900

gccagacaag ataaatcaag cagattatgc actggatgct gcggtgactc 950

ttctagaatt ttatgaggat tatttcagca taccgtatcc cctacccaaa 1000

caagatcttg ctgctattcc cgactttcag tctggtgcta tggaaaactg 1050

gggactgaca acatatagag aatctgctct gttgtttgat gcagaaagt 1100

cttctgcatc aagtaagctt ggcatcacag tgactgtggc ccatgaactg 1150

gcccaccagt ggtttgggaa cctggtcact atggaatggt ggaatgatct 1200

ttggctaaat gaaggatttg ccaaatttat ggagtttgtg tctgtcagtg 1250

tgacccatcc tgaactgaaa gttggagatt atttctttgg caaatgtttt 1300

gacgcaatgg aggtagatgc tttaaattcc tcacaccctg tgtctacacc 1350

tgtggaaaat cctgctcaga tccgggagat gtttgatgat gtttcttatg 1400

ataagggagc ttgtattctg aatatgctaa gggagtatct tagcgctgac 1450

gcatttaaaa gtggtattgt acagtatctc cagaagcata gctataaaaa 1500

tacaaaaaac gaggacctgt gggatagtat ggcaagtatt tgccctacag 1550

atggtgtaaa agggatggat ggcttttgct ctagaagtca acattcatct 1600

tcatcctcac attggcatca ggaaggggtg gatgtgaaaa ccatgatgaa 1650

cacttggaca ctgcagaggg gtttttcccct aataaccatc acagtgaggg 1700

ggaggaatgt acacatgaag caagagcact acatgaaggg ctctgacggc 1750

gccccggaca ctgggtacct gtggcatgtt ccattgacat tcatcaccag 1800

caaatccaac atggtccatc gatttttgct aaaaacaaaa acagatgtgc 1850

tcatcctccc agaagaggtg gaatggatca aatttaatgt gggcatgaat 1900

ggctattaca ttgtgcatta cgaggatgat ggatgggact ctttgactgg 1950

ccttttaaaa ggaacacaca cagcagtcag cagtaatgat cgggcaagtc 2000

tcattaacaa tgcatttcag ctcgtcagca ttgggaagct gtccattgaa 2050

aaggccttgg atttatccct gtacttgaaa catgaaactg aaattatgcc 2100

cgtgtttcaa ggtttgaatg agctgattcc tatgtataag ttaatggaga 2150

aaagagatat gaatgaagtg gaaactcaat tcaaggcctt cctcatcagg 2200

ctgctaaggg acctcattga taagcagaca tggacagacg agggctcagt 2250

ctcagagcaa atgctgcgga gtgaactact actcctcgcc tgtgtgcaca 2300

333

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actatcagcc gtgcgtacag agggcagaag gctatttcag aaagtggaag 2350

gaatccaatg gaaacttgag cctgcctgtc gacgtgacct tggcagtgtt 2400

tgctgtgggg gcccagagca cagaaggctg ggattttctt tatagtaaat 2450

atcagttttc tttgtccagt actgagaaaa gccaaattga atttgccctc 2500

tgcagaaccc aaaataagga aaagcttcaa tggctactag atgaaagctt 2550

taagggagat aaaataaaaa ctcaggagtt ccacaaatt cttacactca 2600

ttggcaggaa cccagtagga tacccactgg cctggcaatt tctgaggaaa 2650

aactggaaca aacttgtaca aaagtttgaa cttggctcat cttccatagc 2700

ccacatggta atgggtacaa caaatcaatt ctccacaaga acacggcttg 2750

aagaggtaaa aggattcttc agctctttga aagaaaatgg ttctcagctc 2800

cgttgtgtcc aacagacaat tgaaaccatt gaagaaaaca tcggttggat 2850

ggataagaat tttgataaaa tcagagtgtg gctgcaaagt gaaaagcttg 2900

aacgtatgta aaaattcctc ccttgcccgg ttcctgttat ctctaatcac 2950

caacattttg ttgagtgtat tttcaaacta gagatggctg ttttggctcc 3000

aactggagat acttttttcc cttcaactca ttttttgact atccctgtga 3050

aaagaatagc tgttagtttt tcatgaatgg gctttttcat gaatgggcta 3100

tcgctaccat gtgttttgtt catcacaggt gttgccctgc aacgtaaacc 3150

caagtgttgg gttccctgcc acagaagaat aaagtacctt attcttctca 3200

aaaaaaaaaa aaaaaaaaaa aaaaaa 3226
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<210> 353
<211> 941
<212> PRT
<213> Homo sapiens

<400> 353
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Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala Thr Met Ser Phe
 1               5                  10                  15

Leu Leu Ser Ser Leu Leu Ala Leu Leu Thr Val Ser Thr Pro Ser
                20                  25                  30

Trp Cys Gln Ser Thr Glu Ala Ser Pro Lys Arg Ser Asp Gly Thr
                35                  40                  45

Pro Phe Pro Trp Asn Lys Ile Arg Leu Pro Glu Tyr Val Ile Pro
                50                  55                  60

Val His Tyr Asp Leu Leu Ile His Ala Asn Leu Thr Thr Leu Thr
                65                  70                  75
```

Phe Trp Gly Thr Thr Lys Val Glu Ile Thr Ala Ser Gln Pro Thr
                80   85   90

Ser Thr Ile Ile Leu His Ser His His Leu Gln Ile Ser Arg Ala
                95   100   105

Thr Leu Arg Lys Gly Ala Gly Glu Arg Leu Ser Glu Glu Pro Leu
               110   115   120

Gln Val Leu Glu His Pro Pro Gln Glu Gln Ile Ala Leu Leu Ala
               125   130   135

Pro Glu Pro Leu Leu Val Gly Leu Pro Tyr Thr Val Val Ile His
               140   145   150

Tyr Ala Gly Asn Leu Ser Glu Thr Phe His Gly Phe Tyr Lys Ser
               155   160   165

Thr Tyr Arg Thr Lys Glu Gly Glu Leu Arg Ile Leu Ala Ser Thr
               170   175   180

Gln Phe Glu Pro Thr Ala Ala Arg Met Ala Phe Pro Cys Phe Asp
               185   190   195

Glu Pro Ala Phe Lys Ala Ser Phe Ser Ile Lys Ile Arg Arg Glu
               200   205   210

Pro Arg His Leu Ala Ile Ser Asn Met Pro Leu Val Lys Ser Val
               215   220   225

Thr Val Ala Glu Gly Leu Ile Glu Asp His Phe Asp Val Thr Val
               230   235   240

Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile Ser Asp Phe Glu
               245   250   255

Ser Val Ser Lys Ile Thr Lys Ser Gly Val Lys Val Ser Val Tyr
               260   265   270

Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu Asp Ala
               275   280   285

Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile Pro
               290   295   300

Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln
               305   310   315

Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser
               320   325   330

Ala Leu Leu Phe Asp Ala Glu Lys Ser Ser Ala Ser Ser Lys Leu
               335   340   345

Gly Ile Thr Val Thr Val Ala His Glu Leu Ala His Gln Trp Phe
               350   355   360

Gly Asn Leu Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn

335

Glu Gly Phe Ala Lys Phe Met Glu Phe Val Ser Val Ser Val Thr
          380   385   390

His Pro Glu Leu Lys Val Gly Asp Tyr Phe Phe Gly Lys Cys Phe
          395   400   405

Asp Ala Met Glu Val Asp Ala Leu Asn Ser Ser His Pro Val Ser
          410   415   420

Thr Pro Val Glu Asn Pro Ala Gln Ile Arg Glu Met Phe Asp Asp
          425   430   435

Val Ser Tyr Asp Lys Gly Ala Cys Ile Leu Asn Met Leu Arg Glu
          440   445   450

Tyr Leu Ser Ala Asp Ala Phe Lys Ser Gly Ile Val Gln Tyr Leu
          455   460   465

Gln Lys His Ser Tyr Lys Asn Thr Lys Asn Glu Asp Leu Trp Asp
          470   475   480

Ser Met Ala Ser Ile Cys Pro Thr Asp Gly Val Lys Gly Met Asp
          485   490   495

Gly Phe Cys Ser Arg Ser Gln His Ser Ser Ser Ser Ser His Trp
          500   505   510

His Gln Glu Gly Val Asp Val Lys Thr Met Met Asn Thr Trp Thr
          515   520   525

Leu Gln Arg Gly Phe Pro Leu Ile Thr Ile Thr Val Arg Gly Arg
          530   535   540

Asn Val His Met Lys Gln Glu His Tyr Met Lys Gly Ser Asp Gly
          545   550   555

Ala Pro Asp Thr Gly Tyr Leu Trp His Val Pro Leu Thr Phe Ile
          560   565   570

Thr Ser Lys Ser Asn Met Val His Arg Phe Leu Leu Lys Thr Lys
          575   580   585

Thr Asp Val Leu Ile Leu Pro Glu Glu Val Glu Trp Ile Lys Phe
          590   595   600

Asn Val Gly Met Asn Gly Tyr Tyr Ile Val His Tyr Glu Asp Asp
          605   610   615

Gly Trp Asp Ser Leu Thr Gly Leu Leu Lys Gly Thr His Thr Ala
          620   625   630

Val Ser Ser Asn Asp Arg Ala Ser Leu Ile Asn Asn Ala Phe Gln
          635   640   645

Leu Val Ser Ile Gly Lys Leu Ser Ile Glu Lys Ala Leu Asp Leu
          650   655   660

```
Ser Leu Tyr Leu Lys His Glu Thr Glu Ile Met Pro Val Phe Gln
                665                 670                 675

Gly Leu Asn Glu Leu Ile Pro Met Tyr Lys Leu Met Glu Lys Arg
                680                 685                 690

Asp Met Asn Glu Val Glu Thr Gln Phe Lys Ala Phe Leu Ile Arg
                695                 700                 705

Leu Leu Arg Asp Leu Ile Asp Lys Gln Thr Trp Thr Asp Glu Gly
                710                 715                 720

Ser Val Ser Glu Gln Met Leu Arg Ser Glu Leu Leu Leu Leu Ala
                725                 730                 735

Cys Val His Asn Tyr Gln Pro Cys Val Gln Arg Ala Glu Gly Tyr
                740                 745                 750

Phe Arg Lys Trp Lys Glu Ser Asn Gly Asn Leu Ser Leu Pro Val
                755                 760                 765

Asp Val Thr Leu Ala Val Phe Ala Val Gly Ala Gln Ser Thr Glu
                770                 775                 780

Gly Trp Asp Phe Leu Tyr Ser Lys Tyr Gln Phe Ser Leu Ser Ser
                785                 790                 795

Thr Glu Lys Ser Gln Ile Glu Phe Ala Leu Cys Arg Thr Gln Asn
                800                 805                 810

Lys Glu Lys Leu Gln Trp Leu Leu Asp Glu Ser Phe Lys Gly Asp
                815                 820                 825

Lys Ile Lys Thr Gln Glu Phe Pro Gln Ile Leu Thr Leu Ile Gly
                830                 835                 840

Arg Asn Pro Val Gly Tyr Pro Leu Ala Trp Gln Phe Leu Arg Lys
                845                 850                 855

Asn Trp Asn Lys Leu Val Gln Lys Phe Glu Leu Gly Ser Ser Ser
                860                 865                 870

Ile Ala His Met Val Met Gly Thr Thr Asn Gln Phe Ser Thr Arg
                875                 880                 885

Thr Arg Leu Glu Glu Val Lys Gly Phe Phe Ser Ser Leu Lys Glu
                890                 895                 900

Asn Gly Ser Gln Leu Arg Cys Val Gln Gln Thr Ile Glu Thr Ile
                905                 910                 915

Glu Glu Asn Ile Gly Trp Met Asp Lys Asn Phe Asp Lys Ile Arg
                920                 925                 930

Val Trp Leu Gln Ser Glu Lys Leu Glu Arg Met
                935                 940
```

<210> 354

<211> 1587
<212> DNA
<213> Homo sapiens

<400> 354
cagccacaga cgggtcatga gcgcggtatt actgctggcc ctcctggggt 50

tcatcctccc actgccagga gtgcaggcgc tgctctgcca gtttgggaca 100

gttcagcatg tgtggaaggt gtccgaccta ccccggcaat ggacccctaa 150

gaacaccagc tgcgacagcg gcttggggtg ccaggacacg ttgatgctca 200

ttgagagcgg accccaagtg agcctggtgc tctccaaggg ctgcacggag 250

gccaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300

ctccctgatc tcctacacct tcgtgtgccg ccaggaggac ttctgcaaca 350

acctcgttaa ctccctcccg ctttgggccc cacagccccc agcagaccca 400

ggatccttga ggtgcccagt ctgcttgtct atggaaggct gtctggaggg 450

gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500

tcctcaggct caggggagga ggcatcttct ccaatctgag agtccaggga 550

tgcatgcccc agccaggttg caacctgctc aatgggacac aggaaattgg 600

gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650

atcgggggac caccattatg acacacggaa acttggctca agaacccact 700

gattggacca catcgaatac cgagatgtgc gaggtggggc aggtgtgtca 750

ggagacgctg ctgctcatag atgtaggact cacatcaacc ctggtgggga 800

caaaaggctg cagcactgtt ggggctcaaa attcccagaa gaccaccatc 850

cactcagccc ctcctggggt gcttgtggcc tcctataccc acttctgctc 900

ctcggacctg tgcaatagtg ccagcagcag cagcgttctg ctgaactccc 950

tccctcctca agctgcccct gtcccaggag accggcagtg tcctacctgt 1000

gtgcagcccc ttggaacctg ttcaagtggc tccccccgaa tgacctgccc 1050

caggggcgcc actcattgtt atgatgggta cattcatctc tcaggaggtg 1100

ggctgtccac caaaatgagc attcagggct gcgtggccca accttccagc 1150

ttcttgttga accacaccag acaaatcggg atcttctctg cgcgtgagaa 1200

gcgtgatgtg cagcctcctg cctctcagca tgagggaggt ggggctgagg 1250

gcctggagtc tctcacttgg ggggtggggc tggcactggc cccagcgctg 1300

tggtggggag tggtttgccc ttcctgctaa ctctattacc cccacgattc 1350

338

ttcaccgctg ctgaccaccc acactcaacc tccctctgac ctcataacct 1400

aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450

cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500

gcctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550

gctgcatgta tctgataata cagaccctgt cctttca 1587

<210> 355
<211> 437
<212> PRT
<213> Homo sapiens

<400> 355

```
Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro
 1               5                  10                  15

Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln
            20                  25                  30

His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys
            35                  40                  45

Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
            50                  55                  60

Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
            65                  70                  75

Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
            80                  85                  90

Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
            95                  100                 105

Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
            110                 115                 120

Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
            125                 130                 135

Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
            140                 145                 150

Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu
            155                 160                 165

Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met
            170                 175                 180

Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly
            185                 190                 195

Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr
            200                 205                 210
```

339

Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln
                215   220   225

Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val
                230   235   240

Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu
                245   250   255

Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala
                260   265   270

Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val
                275   280   285

Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn
                290   295   300

Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln
                305   310   315

Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln
                320   325   330

Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro
                335   340   345

Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly
                350   355   360

Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln
                365   370   375

Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe
                380   385   390

Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His
                395   400   405

Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val
                410   415   420

Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro
                425   430   435

Ser Cys

<210> 356
<211> 1238
<212> DNA
<213> Homo sapiens

<400> 356
 gcgacgggca ggacgccccg ttcgcctagc gcgtgctcag gagttggtgt 50

 cctgcctgcg ctcaggatga gggggaatct ggccctggtg ggcgttctaa 100

340

tcagcctggc cttcctgtca ctgctgccat ctggacatcc tcagccggct 150

ggcgatgacg cctgctctgt gcagatcctc gtccctggcc tcaaagggga 200

tgcgggagag aagggagaca aaggcgcccc cggacggcct ggaagagtcg 250

gccccacggg agaaaaagga gacatggggg acaaaggaca gaaaggcagt 300

gtgggtcgtc atggaaaaat tggtcccatt ggctctaaag gtgagaaagg 350

agattccggt gacataggac ccctggtcc taatggagaa ccaggcctcc 400

catgtgagtg cagccagctg cgcaaggcca tcggggagat ggacaaccag 450

gtctctcagc tgaccagcga gctcaagttc atcaagaatg ctgtcgccgg 500

tgtgcgcgag acggagagca agatctacct gctggtgaag gaggagaagc 550

gctacgcgga cgcccagctg tcctgccagg ccgcggggg cacgctgagc 600

atgcccaagg acgaggctgc caatggcctg atggccgcat acctggcgca 650

agccggcctg gcccgtgtct tcatcggcat caacgacctg gagaaggagg 700

gcgccttcgt gtactctgac cactccccca tgcggacctt caacaagtgg 750

cgcagcggtg agcccaacaa tgcctacgac gaggaggact gcgtggagat 800

ggtggcctcg gcggctgga cgacgtggc ctgccacacc accatgtact 850

tcatgtgtga gtttgacaag gagaacatgt gagcctcagg ctggggctgc 900

ccattggggg ccccacatgt ccctgcaggg ttggcaggga cagagcccag 950

accatggtgc cagccaggga gctgtccctc tgtgaagggt ggaggctcac 1000

tgagtagagg gctgttgtct aaactgagaa aatggcctat gcttaagagg 1050

aaaatgaaag tgttcctggg gtgctgtctc tgaagaagca gagtttcatt 1100

acctgtattg tagccccaat gtcattatgt aattattacc cagaattgct 1150

cttccataaa gcttgtgcct ttgtccaagc tatacaataa aatctttaag 1200

tagtgcagta gttaagtcca aaaaaaaaa aaaaaaa 1238

<210> 357
<211> 271
<212> PRT
<213> Homo sapiens

<400> 357
Met Arg Gly Asn Leu Ala Leu Val Gly Val Leu Ile Ser Leu Ala
1   5   10   15

Phe Leu Ser Leu Leu Pro Ser Gly His Pro Gln Pro Ala Gly Asp
                20   25   30

341

Asp Ala Cys Ser Val Gln Ile Leu Val Pro Gly Leu Lys Gly Asp
           35   40   45

Ala Gly Glu Lys Gly Asp Lys Gly Ala Pro Gly Arg Pro Gly Arg
           50   55   60

Val Gly Pro Thr Gly Glu Lys Gly Asp Met Gly Asp Lys Gly Gln
           65   70   75

Lys Gly Ser Val Gly Arg His Gly Lys Ile Gly Pro Ile Gly Ser
           80   85   90

Lys Gly Glu Lys Gly Asp Ser Gly Asp Ile Gly Pro Pro Gly Pro
           95   100   105

Asn Gly Glu Pro Gly Leu Pro Cys Glu Cys Ser Gln Leu Arg Lys
          110   115   120

Ala Ile Gly Glu Met Asp Asn Gln Val Ser Gln Leu Thr Ser Glu
          125   130   135

Leu Lys Phe Ile Lys Asn Ala Val Ala Gly Val Arg Glu Thr Glu
          140   145   150

Ser Lys Ile Tyr Leu Leu Val Lys Glu Glu Lys Arg Tyr Ala Asp
          155   160   165

Ala Gln Leu Ser Cys Gln Gly Arg Gly Gly Thr Leu Ser Met Pro
          170   175   180

Lys Asp Glu Ala Ala Asn Gly Leu Met Ala Ala Tyr Leu Ala Gln
          185   190   195

Ala Gly Leu Ala Arg Val Phe Ile Gly Ile Asn Asp Leu Glu Lys
          200   205   210

Glu Gly Ala Phe Val Tyr Ser Asp His Ser Pro Met Arg Thr Phe
          215   220   225

Asn Lys Trp Arg Ser Gly Glu Pro Asn Asn Ala Tyr Asp Glu Glu
          230   235   240

Asp Cys Val Glu Met Val Ala Ser Gly Gly Trp Asn Asp Val Ala
          245   250   255

Cys His Thr Thr Met Tyr Phe Met Cys Glu Phe Asp Lys Glu Asn
          260   265   270

Met

<210> 358
<211> 972
<212> DNA
<213> Homo sapiens

<400> 358
 agtgactgca gccttcctag atcccctcca ctcggtttct ctctttgcag 50

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gagcaccggc agcaccagtg tgtgagggga gcaggcagcg gtcctagcca 100

gttccttgat cctgccagac cacccagccc ccggcacaga gctgctccac 150

aggcaccatg aggatcatgc tgctattcac agccatcctg gccttcagcc 200

tagctcagag ctttggggct gtctgtaagg agccacagga ggaggtggtt 250

cctggcgggg gccgcagcaa gagggatcca gatctctacc agctgctcca 300

gagactcttc aaaagccact catctctgga gggattgctc aaagccctga 350

gccaggctag cacagatcct aaggaatcaa catctcccga gaaacgtgac 400

atgcatgact ctttgtgggg acttatgggc aagaggagcg tccagccaga 450

gggaaagaca ggacctttct taccttcagt gagggttcct cggccccttc 500

atcccaatca gcttggatcc acaggaaagt cttccctggg aacagaggag 550

cagagacctt tataagactc tcctacggat gtgaatcaag agaacgtccc 600

cagctttggc atcctcaagt atcccccgag agcagaatag gtactccact 650

tccggactcc tggactgcat taggaagacc tctttccctg tcccaatccc 700

caggtgcgca cgctcctgtt acccttctc ttccctgttc ttgtaacatt 750

cttgtgcttt gactccttct ccatctttc tacctgaccc tggtgtggaa 800

actgcatagt gaatatcccc aaccccaatg ggcattgact gtagaatacc 850

ctagagttcc tgtagtgtcc tacattaaaa atataatgtc tctctctatt 900

cctcaacaat aaaggatttt tgcatatgaa aaaaaaaaa aaaaaaaaa 950

aaaaaaaaaa aaaaaaaaaa aa 972
```

<210> 359
<211> 135
<212> PRT
<213> Homo sapiens

<400> 359
```
Met Arg Ile Met Leu Leu Phe Thr Ala Ile Leu Ala Phe Ser Leu
 1               5                  10                  15

Ala Gln Ser Phe Gly Ala Val Cys Lys Glu Pro Gln Glu Glu Val
                20                  25                  30

Val Pro Gly Gly Gly Arg Ser Lys Arg Asp Pro Asp Leu Tyr Gln
                35                  40                  45

Leu Leu Gln Arg Leu Phe Lys Ser His Ser Ser Leu Glu Gly Leu
                50                  55                  60

Leu Lys Ala Leu Ser Gln Ala Ser Thr Asp Pro Lys Glu Ser Thr
                65                  70                  75
```

343

```
Ser Pro Glu Lys Arg Asp Met His Asp Phe Phe Val Gly Leu Met
            80                  85                      90

Gly Lys Arg Ser Val Gln Pro Glu Gly Lys Thr Gly Pro Phe Leu
            95                 100                     105

Pro Ser Val Arg Val Pro Arg Pro Leu His Pro Asn Gln Leu Gly
           110                 115                     120

Ser Thr Gly Lys Ser Ser Leu Gly Thr Glu Glu Gln Arg Pro Leu
           125                 130                     135
```

<210> 360
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 360
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gggcgtctcc ggctgctcct attgagctgt ctgctcgctg tgcccgctgt 50

gcctgctgtg cccgcgctgt cgccgctgct accgcgtctg ctggacgcgg 100

gagacgccag cgagctggtg attggagccc tgcggagagc tcaagcgccc 150

agctctgccc caggagccca ggctgccccg tgagtcccat agttgctgca 200

ggagtggagc catgagctgc gtcctgggtg gtgtcatccc cttggggctg 250

ctgttcctgg tctgcggatc ccaaggctac ctcctgccca cgtcactct 300

cttagaggag ctgctcagca ataccagca caacgagtct cactcccggg 350

tccgcagagc catccccagg gaggacaagg aggagatcct catgctgcac 400

aacaagcttc ggggccaggt gcagcctcag gcctccaaca tggagtacat 450

ggtgagcgcc ggctccggcc gcagaggctg gcaccggggg tggggcctgg 500

gccaccagcc tgctctgttc cccagccagc tctgttcccc agccagtgcg 550

tgtgatggct ggctcagggt ctcctctggc aggggaggat cccggctctg 600

ttctgttttg tttgtttgtt ttgagacagg gtctcactct gccactgacg 650

ctggagtgca atggcacaat cgtcatgccc tgaaaccta gactcccggg 700

gttaagcgat cctgcttcag cctcccaagt agctggaact acaggcatgc 750

accatggtgc ccagctagat tttaaatatt ttgtggagat gggggtcttg 800

ctacgttgcc caggctggtc ttgaactcct aggctcaagc aatcctcctg 850

cctcagcctc tcaaagtgct aggattatag gcatgagtca ccctgtctgg 900

ctctggctct gttcttaaca ttctgccaaa acaacacacg tgggttccct 950

gtgcagagcc tgcctcgttg ccttcatgtc actcttggta gctccactgg 1000
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344

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gaacacagct ctcagccttt cccacctgga ggcagagtgg ggaggggccc 1050

agggctgggc tttgctgatg ctgatctcag ctgtgccaca cgctagctgc 1100

accaccctga cttctcctta gcccgtgtga gcctcacttt ccacttggag 1150

agtccttcct cgcgtggttg ccatgactgt gagataagtc gaggctgtga 1200

agggcccggc acagactgac ctgcctcccc aaccctagg ctttgctaac 1250

cgggaaagga gctaacggtg acagaagaca gccaaggtca accctcccgg 1300

gtgattgtga tgggtgttcc aggtgtggtt gggcgatgct gctacttgac 1350

cccaagctcc agtgtggaaa cttccttcct ggctggtttt ccagaactac 1400

agaggaatgg accacagtct tccagggtcc ctcctcgtcc accaaccggg 1450

agcctccacc ttggccatcc gtcagctatg aatggctttt taaacaaacc 1500

cacgtcccag cctgggtaac atggtaaagc cccgtctcta caaaaaaatc 1550

caagttagcc gggcatggtg gtgcgcacct gtagtcccag ctgcagtggg 1600

actgaggtgg aggtggaggt gggggtggg agctgaggaa ggaggatcgc 1650

ttgagcctgg gaagtcgagg ctgcagtgag ctgagattgc accactgcac 1700

tccagcctgg gtgacagagc aagaccctgt ctcaaaaa 1738
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<210> 361
<211> 159
<212> PRT
<213> Homo sapiens

<400> 361

Met	Ser	Cys	Val	Leu	Gly	Gly	Val	Ile	Pro	Leu	Gly	Leu	Leu	Phe
1				5					10					15

Leu	Val	Cys	Gly	Ser	Gln	Gly	Tyr	Leu	Leu	Pro	Asn	Val	Thr	Leu
				20					25					30

Leu	Glu	Glu	Leu	Leu	Ser	Lys	Tyr	Gln	His	Asn	Glu	Ser	His	Ser
				35					40					45

Arg	Val	Arg	Arg	Ala	Ile	Pro	Arg	Glu	Asp	Lys	Glu	Glu	Ile	Leu
				50					55					60

Met	Leu	His	Asn	Lys	Leu	Arg	Gly	Gln	Val	Gln	Pro	Gln	Ala	Ser
				65					70					75

Asn	Met	Glu	Tyr	Met	Val	Ser	Ala	Gly	Ser	Gly	Arg	Arg	Gly	Trp
				80					85					90

His	Arg	Gly	Trp	Gly	Leu	Gly	His	Gln	Pro	Ala	Leu	Phe	Pro	Ser
				95					100					105

Gln	Leu	Cys	Ser	Pro	Ala	Ser	Ala	Cys	Asp	Gly	Trp	Leu	Arg	Val

345

Ser Ser Gly Arg Gly Gly Ser Arg Leu Cys Ser Val Leu Phe Val
                125   130   135

Cys Phe Glu Thr Gly Ser His Ser Ala Thr Asp Ala Gly Val Gln
                140   145   150

Trp His Asn Arg His Ala Leu Lys Pro
                155

<210> 362
<211> 422
<212> DNA
<213> Homo sapiens

<400> 362
 aaggagaggc caccgggact tcagtgtctc ctccatccca ggagcgcagt 50

 ggccactatg gggtctgggc tgccccttgt cctcctcttg accctccttg 100

 gcagctcaca tggaacaggg ccgggtatga ctttgcaact gaagctgaag 150

 gagtcttttc tgacaaattc ctcctatgag tccagcttcc tggaattgct 200

 tgaaaagctc tgcctcctcc tccatctccc ttcagggacc agcgtcaccc 250

 tccaccatgc aagatctcaa caccatgttg tctgcaacac atgacagcca 300

 ttgaagcctg tgtccttctt ggcccgggct tttgggccgg ggatgcagga 350

 ggcaggcccc gaccctgtct ttcagcaggc ccccaccctc ctgagtggca 400

 ataaataaaa ttcggtatgc tg 422

<210> 363
<211> 78
<212> PRT
<213> Homo sapiens

<400> 363
 Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly
   1   5   10   15

 Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu
                20   25   30

 Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu
                35   40   45

 Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
                50   55   60

 Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val
                65   70   75

 Cys Asn Thr

<210> 364
<211> 826
<212> DNA
<213> Homo sapiens

<400> 364
aattgtatct gtgtaatgtt aaaacaaacg aaataaaata gaaggaaaaa 50

ctttctgagt ttcaaaaaca acagactagt actctaaaga actctttaaa 100

acaattaact gttaggattg cagttatgat tggatattat ttaattctgt 150

ttctgatgtg gggttcctcc actgtgttct gtgtgctatt aatatttacc 200

attgcagaag cttcattcag tgttgaaaat gaatgcttag tggatctgtg 250

cctcttacgc atatgttaca aattatctgg agttcctaat caatgcagag 300

ttcccctccc ctccgattgt tctaaataat tgaaagatgt ctgctgtgga 350

aaaaggcatg tatttaaatc tgtatgattc tcaaccatct ttagttggga 400

aaggtccttg aaagccaatg gaaatacttt ttttttttct tggcactaat 450

caagtgagtg ttaccttttc acttagtagg atgtgttgtt acgctagtaa 500

aatagaaacc tgtgtttatt ctcaggtatt ttagaaacaa cagccatcat 550

tttattttat gtgtgtgttc ttggctgtat tcataaatta tatattttgg 600

gctatcaaat attacttcat tcaatataaa taacaatagt agaagttgtt 650

tacttagata tgctttctag ttgcattttc tcagcctatg taagactact 700

ttgttgtaat agcctttgaa atttacagta ctgtctctct actatcttca 750

gattacttga ttcaaataaa ccaattatgt ttgtaattga tattaataaa 800

accagaataa aagttcatat ctaccc 826

<210> 365
<211> 67
<212> PRT
<213> Homo sapiens

<400> 365
Met Ile Gly Tyr Tyr Leu Ile Leu Phe Leu Met Trp Gly Ser Ser
1   5   10   15

Thr Val Phe Cys Val Leu Leu Ile Phe Thr Ile Ala Glu Ala Ser
                20   25   30

Phe Ser Val Glu Asn Glu Cys Leu Val Asp Leu Cys Leu Leu Arg
                35   40   45

Ile Cys Tyr Lys Leu Ser Gly Val Pro Asn Gln Cys Arg Val Pro
                50   55   60

347

Leu Pro Ser Asp Cys Ser Lys
                65

<210> 366
<211> 2475
<212> DNA
<213> Homo sapiens

<400> 366
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 tgagacatcc ttgagaagag ccacagcata agagactgcc ctgcttggtg 100

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 gttccttgca gcttttctgc ccccgccgca gtgtacccag acccagcca 200

 tggtgcatta catctaccag cgctttcgag tcttggagca agggctggaa 250

 aaatgtaccc aagcaacgag ggcatacatt caagaattcc aagagttctc 300

 aaaaaatata tctgtcatgc tgggaagatg tcagacctac acaagtgagt 350

 acaagagtgc agtgggtaac ttggcactga gagttgaacg tgcccaacgg 400

 gagattgact acatacaata ccttcgagag gctgacgagt gcatcgtatc 450

 agaggacaag acactggcag aaatgttgct ccaagaagct gaagaagaga 500

 aaaagatccg gactctgctg aatgcaagct gtgacaacat gctgatgggc 550

 ataaagtctt tgaaaatagt gaagaagatg atggacacac atggctcttg 600

 gatgaaagat gctgtctata actctccaaa ggtgtactta ttaattggat 650

 ccagaaacaa cactgtttgg gaatttgcaa acatacgggc attcatggag 700

 gataacacca agccagctcc ccggaagcaa atcctaacac tttcctggca 750

 gggaacaggc caagtgatct acaaaggttt tctatttttt cataaccaag 800

 caacttctaa tgagataatc aaatataacc tgcagaagag gactgtggaa 850

 gatcgaatgc tgctcccagg aggggtaggc cgagcattgg tttaccagca 900

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 gagccgggca cactgggagt ggagcattca tgggataccc catgcagaag 1050

 ccaggatgct gaagcctcat tcctcttgtg tggggttctc tatgtggtct 1100

 acagtactgg gggccagggc cctcatcgca tcacctgcat ctatgatcca 1150

 ctgggcacta tcagtgagga ggacttgccc aacttgttct tccccaagag 1200

 accaagaagt cactccatga tccattacaa ccccagagat aagcagctct 1250

                            348

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atgcctggaa tgaaggaaac cagatcattt acaaactcca gacaaagaga 1300

aagctgcctc tgaagtaatg cattacagct gtgagaaaga gcactgtggc 1350

tttggcagct gttctacagg acagtgaggc tatagcccct tcacaatata 1400

gtatccctct aatcacacac aggaagagtg tgtagaagtg gaaatacgta 1450

tgcctccttt cccaaatgtc actgccttag gtatcttcca agagcttaga 1500

tgagagcata tcatcaggaa agtttcaaca atgtccatta ctcccccaaa 1550

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tgggattaca ggcatgtgcc accacacctg gcttaaaata ctatttctta 1950

ttgaggttta acctctattt cccctagccc tgtccttcca ctaagcttgg 2000

tagatgtaat aataaagtga aaatattaac atttgaatat cgctttccag 2050

gtgtggagtg tttgcacatc attgaattct cgtttcacct ttgtgaaaca 2100

tgcacaagtc tttacagctg tcattctaga gtttaggtga gtaacacaat 2150

tacaaagtga aagatacagc tagaaaatac tacaaatccc atagttttttc 2200

cattgcccaa ggaagcatca aatacgtatg tttgttcacc tactcttata 2250

gtcaatgcgt tcatcgtttc agcctaaaaa taatagtctg tccctttagc 2300

cagttttcat gtctgcacaa gacctttcaa taggcctttc aaatgataat 2350

tcctccagaa aaccagtcta agggtgagga ccccaactct agcctcctct 2400

tgtcttgctg tcctctgttt ctctctttct gctttaaatt caataaaagt 2450

gacactgagc aaaaaaaaaa aaaaa 2475
```

<210> 367
<211> 402
<212> PRT
<213> Homo sapiens

<400> 367
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Met Met Val Ala Leu Arg Gly Ala Ser Ala Leu Leu Val Leu Phe
1               5                   10                  15
```

349

Leu Ala Ala Phe Leu Pro Pro Pro Gln Cys Thr Gln Asp Pro Ala
          20   25   30

Met Val His Tyr Ile Tyr Gln Arg Phe Arg Val Leu Glu Gln Gly
          35   40   45

Leu Glu Lys Cys Thr Gln Ala Thr Arg Ala Tyr Ile Gln Glu Phe
          50   55   60

Gln Glu Phe Ser Lys Asn Ile Ser Val Met Leu Gly Arg Cys Gln
          65   70   75

Thr Tyr Thr Ser Glu Tyr Lys Ser Ala Val Gly Asn Leu Ala Leu
          80   85   90

Arg Val Glu Arg Ala Gln Arg Glu Ile Asp Tyr Ile Gln Tyr Leu
          95   100   105

Arg Glu Ala Asp Glu Cys Ile Val Ser Glu Asp Lys Thr Leu Ala
          110   115   120

Glu Met Leu Leu Gln Glu Ala Glu Glu Lys Lys Ile Arg Thr
          125   130   135

Leu Leu Asn Ala Ser Cys Asp Asn Met Leu Met Gly Ile Lys Ser
          140   145   150

Leu Lys Ile Val Lys Lys Met Met Asp Thr His Gly Ser Trp Met
          155   160   165

Lys Asp Ala Val Tyr Asn Ser Pro Lys Val Tyr Leu Leu Ile Gly
          170   175   180

Ser Arg Asn Asn Thr Val Trp Glu Phe Ala Asn Ile Arg Ala Phe
          185   190   195

Met Glu Asp Asn Thr Lys Pro Ala Pro Arg Lys Gln Ile Leu Thr
          200   205   210

Leu Ser Trp Gln Gly Thr Gly Gln Val Ile Tyr Lys Gly Phe Leu
          215   220   225

Phe Phe His Asn Gln Ala Thr Ser Asn Glu Ile Ile Lys Tyr Asn
          230   235   240

Leu Gln Lys Arg Thr Val Glu Asp Arg Met Leu Leu Pro Gly Gly
          245   250   255

Val Gly Arg Ala Leu Val Tyr Gln His Ser Pro Ser Thr Tyr Ile
          260   265   270

Asp Leu Ala Val Asp Glu His Gly Leu Trp Ala Ile His Ser Gly
          275   280   285

Pro Gly Thr His Ser His Leu Val Leu Thr Lys Ile Glu Pro Gly
          290   295   300

Thr Leu Gly Val Glu His Ser Trp Asp Thr Pro Cys Arg Ser Gln

```
Asp Ala Glu Ala Ser Phe Leu Leu Cys Gly Val Leu Tyr Val Val
                320                325                    330

Tyr Ser Thr Gly Gly Gln Gly Pro His Arg Ile Thr Cys Ile Tyr
                335                340                    345

Asp Pro Leu Gly Thr Ile Ser Glu Glu Asp Leu Pro Asn Leu Phe
                350                355                    360

Phe Pro Lys Arg Pro Arg Ser His Ser Met Ile His Tyr Asn Pro
                365                370                    375

Arg Asp Lys Gln Leu Tyr Ala Trp Asn Glu Gly Asn Gln Ile Ile
                380                385                    390

Tyr Lys Leu Gln Thr Lys Arg Lys Leu Pro Leu Lys
                395                400
```

<210> 368
<211> 2281
<212> DNA
<213> Homo sapiens

<400> 368
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gggcgcccgc gtactcacta gctgaggtgg cagtggttcc accaacatgg  50

agctctcgca gatgtcggag ctcatggggc tgtcggtgtt gcttgggctg  100

ctggccctga tggcgacggc ggcggtagcg cgggggtggc tgcgcgcggg  150

ggaggagagg agcggccggc ccgcctgcca aaaagcaaat ggatttccac  200

ctgacaaatc ttcgggatcc aagaagcaga aacaatatca gcggattcgg  250

aaggagaagc ctcaacaaca caacttcacc caccgcctcc tggctgcagc  300

tctgaagagc cacagcggga acatatcttg catggacttt agcagcaatg  350

gcaaatacct ggctacctgt gcagatgatc gcaccatccg catctggagc  400

accaaggact tcctgcagcg agagcaccgc agcatgagag ccaacgtgga  450

gctggaccac gccaccctgg tgcgcttcag ccctgactgc agagccttca  500

tcgtctggct ggccaacggg gacaccctcc gtgtcttcaa gatgaccaag  550

cgggaggatg ggggctacac cttcacagcc accccagagg acttccctaa  600

aaagcacaag gcgcctgtca tcgacattgg cattgctaac acagggaagt  650

ttatcatgac tgcctccagt gacaccactg tcctcatctg gagcctgaag  700

ggtcaagtgc tgtctaccat caacaccaac cagatgaaca cacacacgc   750

tgctgtatct ccctgtggca gatttgtagc ctcgtgtggc ttcacccccag 800
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351

atgtgaaggt ttgggaagtc tgctttggaa agaagggggga gttccaggag 850

gtggtgcgag ccttcgaact aaagggccac tccgcggctg tgcactcgtt 900

tgctttctcc aacgactcac ggaggatggc ttctgtctcc aaggatggta 950

catggaaact gtgggacaca gatgtggaat acaagaagaa gcaggacccc 1000

tacttgctga agacaggccg ctttgaagag gcggcgggtg ccgcgccgtg 1050

ccgcctggcc ctctccccca acgcccaggt cttggccttg gccagtggca 1100

gtagtattca tctctacaat acccggcggg gcgagaagga ggagtgcttt 1150

gagcgggtcc atggcgagtg tatcgccaac ttgtcctttg acatcactgg 1200

ccgctttctg gcctcctgtg gggaccgggc ggtgcggctg tttcacaaca 1250

ctcctggcca ccgagccatg gtggaggaga tgcagggcca cctgaagcgg 1300

gcctccaacg agagcacccg ccagaggctg cagcagcagc tgacccaggc 1350

ccaagagacc ctgaagagcc tgggtgccct gaagaagtga ctctgggagg 1400

gcccggcgca gaggattgag gaggagggat ctggcctcct catggcactg 1450

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aggtctctct cttcttgctg gctgtgactc ctccctgact agtggccaag 1600

gtgcttttct tcctcccagg cccagtgggt ggaatctgtc cccacctggc 1650

actgaggaga atggtagaga ggagaggaga gagagagaga atgtgatttt 1700

tggccttgtg gcagcacatc ctcacaccca aagaagtttg taaatgttcc 1750

agaacaacct agagaacacc tgagtactaa gcagcagttt tgcaaggatg 1800

ggagactggg atagcttccc atcacagaac tgtgttccat caaaaagaca 1850

ctaagggatt tccttctggg cctcagttct atttgtaaga tggagaataa 1900

tcctctctgt gaactccttg caaagatgat atgaggctaa gagaatatca 1950

agtccccagg tctggaagaa aagtagaaaa gagtagtact attgtccaat 2000

gtcatgaaag tggtaaaagt gggaaccagt gtgctttgaa accaaattag 2050

aaacacattc cttgggaagg caaagttttc tgggacttga tcatacattt 2100

tatatggttg ggacttctct cttcgggaga tgatatcttg tttaaggaga 2150

cctctttttca gttcatcaag ttcatcagat atttgagtgc ccactctgtg 2200

cccaaataaa tatgagctgg ggattaaaaa aaaaaaaaaa aaaaaaaaaa 2250

352

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2281

<210> 369
<211> 447
<212> PRT
<213> Homo sapiens

<400> 369

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Met Glu Leu Ser Gln Met Ser Glu Leu Met Gly Leu Ser Val Leu
  1               5                  10                  15

Leu Gly Leu Leu Ala Leu Met Ala Thr Ala Ala Val Ala Arg Gly
             20                  25                  30

Trp Leu Arg Ala Gly Glu Glu Arg Ser Gly Arg Pro Ala Cys Gln
             35                  40                  45

Lys Ala Asn Gly Phe Pro Pro Asp Lys Ser Ser Gly Ser Lys Lys
             50                  55                  60

Gln Lys Gln Tyr Gln Arg Ile Arg Lys Glu Lys Pro Gln Gln His
             65                  70                  75

Asn Phe Thr His Arg Leu Leu Ala Ala Ala Leu Lys Ser His Ser
             80                  85                  90

Gly Asn Ile Ser Cys Met Asp Phe Ser Ser Asn Gly Lys Tyr Leu
             95                 100                 105

Ala Thr Cys Ala Asp Asp Arg Thr Ile Arg Ile Trp Ser Thr Lys
            110                 115                 120

Asp Phe Leu Gln Arg Glu His Arg Ser Met Arg Ala Asn Val Glu
            125                 130                 135

Leu Asp His Ala Thr Leu Val Arg Phe Ser Pro Asp Cys Arg Ala
            140                 145                 150

Phe Ile Val Trp Leu Ala Asn Gly Asp Thr Leu Arg Val Phe Lys
            155                 160                 165

Met Thr Lys Arg Glu Asp Gly Gly Tyr Thr Phe Thr Ala Thr Pro
            170                 175                 180

Glu Asp Phe Pro Lys Lys His Lys Ala Pro Val Ile Asp Ile Gly
            185                 190                 195

Ile Ala Asn Thr Gly Lys Phe Ile Met Thr Ala Ser Ser Asp Thr
            200                 205                 210

Thr Val Leu Ile Trp Ser Leu Lys Gly Gln Val Leu Ser Thr Ile
            215                 220                 225

Asn Thr Asn Gln Met Asn Asn Thr His Ala Ala Val Ser Pro Cys
            230                 235                 240

Gly Arg Phe Val Ala Ser Cys Gly Phe Thr Pro Asp Val Lys Val
            245                 250                 255
```

353

```
Trp Glu Val Cys Phe Gly Lys Lys Gly Glu Phe Gln Glu Val Val
              260                 265                 270

Arg Ala Phe Glu Leu Lys Gly His Ser Ala Ala Val His Ser Phe
              275                 280                 285

Ala Phe Ser Asn Asp Ser Arg Arg Met Ala Ser Val Ser Lys Asp
              290                 295                 300

Gly Thr Trp Lys Leu Trp Asp Thr Asp Val Glu Tyr Lys Lys Lys
              305                 310                 315

Gln Asp Pro Tyr Leu Leu Lys Thr Gly Arg Phe Glu Glu Ala Ala
              320                 325                 330

Gly Ala Ala Pro Cys Arg Leu Ala Leu Ser Pro Asn Ala Gln Val
              335                 340                 345

Leu Ala Leu Ala Ser Gly Ser Ser Ile His Leu Tyr Asn Thr Arg
              350                 355                 360

Arg Gly Glu Lys Glu Glu Cys Phe Glu Arg Val His Gly Glu Cys
              365                 370                 375

Ile Ala Asn Leu Ser Phe Asp Ile Thr Gly Arg Phe Leu Ala Ser
              380                 385                 390

Cys Gly Asp Arg Ala Val Arg Leu Phe His Asn Thr Pro Gly His
              395                 400                 405

Arg Ala Met Val Glu Glu Met Gln Gly His Leu Lys Arg Ala Ser
              410                 415                 420

Asn Glu Ser Thr Arg Gln Arg Leu Gln Gln Gln Leu Thr Gln Ala
              425                 430                 435

Gln Glu Thr Leu Lys Ser Leu Gly Ala Leu Lys Lys
              440                 445
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<210> 370
<211> 1415
<212> DNA
<213> Homo sapiens

<400> 370

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 tggcctcccc agcttgccag gcacaaggct gagcgggagg aagcgagagg 50

 catctaagca ggcagtgttt tgccttcacc ccaagtgacc atgagaggtg 100

 ccacgcgagt ctcaatcatg ctcctcctag taactgtgtc tgactgtgct 150

 gtgatcacag gggcctgtga gcgggatgtc cagtgtgggg caggcacctg 200

 ctgtgccatc agcctgtggc ttcgagggct gcggatgtgc accccgctgg 250

 ggcgggaagg cgaggagtgc caccccggca gccacaaggt ccccttcttc 300

 aggaaacgca agcaccacac ctgtccttgc ttgcccaacc tgctgtgctc 350
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354

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caggttcccg dacggcaggt accgctgctc catggacttg aagaacatca 400

atttttaggc gcttgcctgg tctcaggata cccaccatcc ttttcctgag 450

cacagcctgg attttattt ctgccatgaa acccagctcc catgactctc 500

ccagtccta cactgactac cctgatctct cttgtctagt acgcacatat 550

gcacacaggc agacatacct cccatcatga catggtcccc aggctggcct 600

gaggatgtca cagcttgagg ctgtggtgtg aaaggtggcc agcctggttc 650

tcttccctgc tcaggctgcc agagaggtgg taaatggcag aaaggacatt 700

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tccccacatg tatccctcgg tctgaattag acattcctgg gcacaggctc 800

ttgggtgcat tgctcagagt cccaggtcct ggcctgaccc tcaggccctt 850

cacgtgaggt ctgtgaggac caatttgtgg gtagttcatc ttccctcgat 900

tggttaactc cttagtttca gaccacagac tcaagattgg ctcttcccag 950

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ctgagagcag gttggtgact ttgaggaggg cagtcctctg tccagattgg 1300

ggtgggagca agggacaggg agcagggcag gggctgaaag gggcactgat 1350

tcagaccagg gaggcaacta cacaccaaca tgctggcttt agaataaaag 1400

caccaactga aaaaa 1415
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<210> 371
<211> 105
<212> PRT
<213> Homo sapiens

<400> 371

Met	Arg	Gly	Ala	Thr	Arg	Val	Ser	Ile	Met	Leu	Leu	Leu	Val	Thr
1				5					10					15

Val	Ser	Asp	Cys	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val
			20					25						30

Gln	Cys	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg
				35				40						45

355

Gly Leu Arg Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys
              50   55   60

His Pro Gly Ser His Lys Val Pro Phe Phe Arg Lys Arg Lys His
              65   70   75

His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro
              80   85   90

Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn Phe
              95   100   105

<210> 372
<211> 1281
<212> DNA
<213> Homo sapiens

<400> 372
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gaaatgtctt tcctccagga cccaagtttc ttcaccatgg ggatgtggtc 100

cattggtgca ggagccctgg gggctgctgc cttggcattg ctgcttgcca 150

acacagacgt gtttctgtcc aagccccaga agcggccct ggagtacctg 200

gaggatatag acctgaaaac actggagaag gaaccaagga ctttcaaagc 250

aaaggagcta tgggaaaaaa atggagctgt gattatggcc gtgcggaggc 300

caggctgttt cctctgtcga gaggaagctg cggatctgtc ctccctgaaa 350

agcatgttgg accagctggg cgtccccctc tatgcagtgg taaaggagca 400

catcaggact gaagtgaagg atttccagcc ttatttcaaa ggagaaatct 450

tcctggatga aaagaaaaag ttctatggtc cacaaaggcg gaagatgatg 500

tttatgggat ttatccgtct gggagtgtgg tacaacttct tccgagcctg 550

gaacggaggc ttctctggaa acctggaagg agaaggcttc atccttgggg 600

gagtttttcgt ggtgggatca ggaaagcagg gcattcttct tgagcaccga 650

gaaaaagaat ttggagacaa agtaaaccta ctttctgttc tggaagctgc 700

taagatgatc aaaccacaga ctttggcctc agagaaaaaa tgattgtgtg 750

aaactgccca gctcagggat aaccagggac attcacctgt gttcatggga 800

tgtattgttt ccactcgtgt ccctaaggag tgagaaaccc atttatactc 850

tactctcagt atggattatt aatgtatttt aatattctgt ttaggcccac 900

taaggcaaaa tagcccccaaa acaagactga caaaaatctg aaaaactaat 950

gaggattatt aagctaaaac ctgggaaata ggaggcttaa aattgactgc 1000

356

caggctgggt gcagtggctc acacctgtaa tcccagcact ttgggaggcc 1050

aaggtgagca agtcacttga ggtcgggagt cgagaccag cctgagcaac 1100

atggcgaaac cccgtctcta ctaaaaatac aaaaatcacc cgggtgtggt 1150

ggcaggcacc tgtagtccca gctacccggg aggctgaggc aggagaatca 1200

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ttccagcctg ggtgactgag actctaacta a 1281

<210> 373
<211> 229
<212> PRT
<213> Homo sapiens

<400> 373
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Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp
 1               5                  10                  15

Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu
                20                  25                  30

Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
                35                  40                  45

Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu
                50                  55                  60

Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala
                65                  70                  75

Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu
                80                  85                  90

Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
                95                  100                 105

Gly Val Pro Leu Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu
                110                 115                 120

Val Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp
                125                 130                 135

Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys Met Met Phe
                140                 145                 150

Met Gly Phe Ile Arg Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala
                155                 160                 165

Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly Glu Gly Phe Ile
                170                 175                 180

Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln Gly Ile Leu
                185                 190                 195

Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn Leu Leu
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357

Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu Ala
                    215   220   225

Ser Glu Lys Lys

<210> 374
<211> 744
<212> DNA
<213> Homo sapiens

<400> 374
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 gccacccagc ccatggcgaa ccccgggctg gggctgcttc tggcgctggg 200

 cctgccgttc ctgctggccc gctggggccg agcctggggg caaatacaga 250

 ccacttctgc aaatgagaat agcactgttt tgccttcatc caccagctcc 300

 agctccgatg gcaacctgcg tccggaagcc atcactgcta tcatcgtggt 350

 cttctccctc ttggctgcct tgctcctggc tgtggggctg gcactgttgg 400

 tgcggaagct tcgggagaag cggcagacgg agggcaccta ccggcccagt 450

 agcgaggagc agttctccca tgcagccgag gcccgggccc ctcaggactc 500

 caaggagacg gtgcagggct gcctgcccat ctaggtcccc tctcctgcat 550

 ctgtctccct tcattgctgt gtgaccttgg ggaaaggcag tgccctctct 600

 gggcagtcag atccacccag tgcttaatag cagggaagaa ggtacttcaa 650

 agactctgcc cctgaggtca agagaggatg gggctattca cttttatata 700

 tttatataaa attagtagtg agatgtaaaa aaaaaaaaaa aaaa 744

<210> 375
<211> 123
<212> PRT
<213> Homo sapiens

<400> 375
 Met Ala Asn Pro Gly Leu Gly Leu Leu Leu Ala Leu Gly Leu Pro
  1   5   10   15

 Phe Leu Leu Ala Arg Trp Gly Arg Ala Trp Gly Gln Ile Gln Thr
                20   25   30

 Thr Ser Ala Asn Glu Asn Ser Thr Val Leu Pro Ser Ser Thr Ser
                35   40   45

Ser Ser Ser Asp Gly Asn Leu Arg Pro Glu Ala Ile Thr Ala Ile
            50   55   60

Ile Val Val Phe Ser Leu Leu Ala Ala Leu Leu Leu Ala Val Gly
            65   70   75

Leu Ala Leu Leu Val Arg Lys Leu Arg Glu Lys Arg Gln Thr Glu
            80   85   90

Gly Thr Tyr Arg Pro Ser Ser Glu Glu Gln Phe Ser His Ala Ala
            95   100   105

Glu Ala Arg Ala Pro Gln Asp Ser Lys Glu Thr Val Gln Gly Cys
            110   115   120

Leu Pro Ile

<210> 376
<211> 713
<212> DNA
<213> Homo sapiens

<400> 376
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 aacatttggg ttttgggatt ttaattttca aacacagcag aatgacattt 100

 tttctgtcac tattattatt gttggtatgt gaagctattt ggagatccaa 150

 ttcaggaagc aacacattgg agaatggcta ctttctatca agaaataaag 200

 agaaccacag tcaacccaca caatcatctt tagaagacag tgtgactcct 250

 accaaagctg tcaaaaccac aggcaagggc atagttaaag gacggaatct 300

 tgactcaaga gggttaattc ttggtgctga gcctggggc aggggtgtaa 350

 agaaaaacac ttagattcaa tgattgtaaa tttaaggcaa atacacatat 400

 tagtattacc ttagtgtaat gtatccctgt catatataca ataaggtgaa 450

 attataagta ccctatgcag ttggctggac agttctaaat tggactttat 500

 taatttttaa aatcagtaac tgatttatca ctggctatgt gcttagatct 550

 acaggagatc atataatttg atacaaataa aagaaaagtg ttctctcccc 600

 ttacagaatt gacattttaa atgcgataca gttagaatag gaaatatgac 650

 attagaaagg aagaatgaca gggagaaagg aaagaaggga aaatgttgcc 700

 aaggaaaaaa aaa 713

<210> 377
<211> 90
<212> PRT
<213> Homo sapiens

<400> 377
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Met Thr Phe Phe Leu Ser Leu Leu Leu Leu Leu Val Cys Glu Ala
 1               5                  10                  15

Ile Trp Arg Ser Asn Ser Gly Ser Asn Thr Leu Glu Asn Gly Tyr
                20                  25                  30

Phe Leu Ser Arg Asn Lys Glu Asn His Ser Gln Pro Thr Gln Ser
                35                  40                  45

Ser Leu Glu Asp Ser Val Thr Pro Thr Lys Ala Val Lys Thr Thr
                50                  55                  60

Gly Lys Gly Ile Val Lys Gly Arg Asn Leu Asp Ser Arg Gly Leu
                65                  70                  75

Ile Leu Gly Ala Glu Ala Trp Gly Arg Gly Val Lys Lys Asn Thr
                80                  85                  90
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<210> 378
<211> 3265
<212> DNA
<213> Homo sapiens

<400> 378
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tgaataataa tggctttgaa gatattgtca ttgttataga tcctagtgtg 150
ccagaagatg aaaaaataat tgaacaaata gaggatatgg tgactacagc 200
ttctacgtac ctgtttgaag ccacagaaaa aagatttttt ttcaaaaatg 250
tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg 300
ccaaaacatg aaaaccataa acatgctgat gttatagttg caccacctac 350
actcccaggt agagatgaac catacaccaa gcagttcaca gaatgtggag 400
agaaaggcga atacattcac ttcacccctg accttctact tggaaaaaaa 450
caaaatgaat atggaccacc aggcaaactg tttgtccatg agtgggctca 500
cctccggtgg ggagtgtttg atgagtacaa tgaagatcag cctttctacc 550
gtgctaagtc aaaaaaaatc gaagcaacaa ggtgttccgc aggtatctct 600
ggtagaaata gagtttataa gtgtcaagga ggcagctgtc ttagtagagc 650
atgcagaatt gattctacaa caaaactgta tggaaaagat tgtcaattct 700
ttcctgataa agtacaaaca gaaaaagcat ccataatgtt tatgcaaagt 750
attgattctg ttgttgaatt ttgtaacgaa aaaacccata atcaagaagc 800
tccaagccta caaaacataa agtgcaattt tagaagtaca tgggaggtga 850
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tgaatcaagc agcaaaacat ttcctgctgc agactgttga aaatggatcc 1050

tgggtgggga tggttcactt tgatagtact gccactattg taaataagct 1100

aatccaaata aaaagcagtg atgaaagaaa cacactcatg gcaggattac 1150

ctacatatcc tctgggagga acttccatct gctctggaat taaatatgca 1200

tttcaggtga ttggagagct acattcccaa ctcgatggat ccgaagtact 1250

gctgctgact gatggggagg ataacactgc aagttcttgt attgatgaag 1300

tgaaacaaag tggggccatt gttcatttta ttgctttggg aagagctgct 1350

gatgaagcag taatagagat gagcaagata acaggaggaa gtcattttta 1400

tgtttcagat gaagctcaga acaatggcct cattgatgct tttggggctc 1450

ttacatcagg aaatactgat ctctcccaga agtcccttca gctcgaaagt 1500

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tgcaaaggtg ggcacttggg catacaatct tcaagccaaa gcgaacccag 1750

aaacattaac tattacagta acttctcgag cagcaaattc ttctgtgcct 1800

ccaatcacag tgaatgctaa aatgaataag gacgtaaaca gtttcccccag 1850

cccaatgatt gtttacgcag aaattctaca aggatatgta cctgttcttg 1900

gagccaatgt gactgctttc attgaatcac agaatggaca tacagaagtt 1950

ttggaacttt tggataatgg tgcaggcgct gattctttca agaatgatgg 2000

agtctactcc aggtatttta cagcatatac agaaaatggc agatatagct 2050

taaaagttcg ggctcatgga ggagcaaaca ctgccaggct aaaattacgg 2100

cctccactga atagagccgc gtacatacca ggctgggtag tgaacgggga 2150

aattgaagca aacccgccaa gacctgaaat tgatgaggat actcagacca 2200

ccttggagga tttcagccga acagcatccg gaggtgcatt tgtggtatca 2250

caagtcccaa gccttccctt gcctgaccaa tacccaccaa gtcaaatcac 2300
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361

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agaccttgat gccacagttc atgaggataa gattattctt acatggacag 2350

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ataagtgcaa gtattcttga tctaagagac agttttgatg atgctcttca 2450

agtaaatact actgatctgt caccaaagga ggccaactcc aaggaaagct 2500

ttgcatttaa accagaaaat atctcagaag aaaatgcaac ccacatattt 2550

attgccatta aaagtataga taaaagcaat ttgacatcaa aagtatccaa 2600

cattgcacaa gtaactttgt ttatccctca agcaaatcct gatgacattg 2650

atcctacacc tactcctact cctactccta ctcctgataa aagtcataat 2700

tctggagtta atatttctac gctggtattg tctgtgattg ggtctgttgt 2750

aattgttaac tttatttaa gtaccaccat ttgaacctta acgaagaaaa 2800

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gtaaaggata tttctgaatc ttaaaattca tcccatgtgt gatcataaac 2900

tcataaaaat aattttaaga tgtcggaaaa ggatactttg attaaataaa 2950

aacactcatg gatatgtaaa aactgtcaag attaaaattt aatagtttca 3000

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gatatttcaa attgcatcaa gaaattaaaa tcatctatct gagtagtcaa 3150

aatacaagta aaggagagca aataaacaac atttggaaaa aaaaaaaaaa 3200

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3250

aaaaaaaaaa aaaaa 3265
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<210> 379
<211> 919
<212> PRT
<213> Homo sapiens

<400> 379

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Met Gly Leu Phe Arg Gly Phe Val Phe Leu Leu Val Leu Cys Leu
1               5                   10                  15

Leu His Gln Ser Asn Thr Ser Phe Ile Lys Leu Asn Asn Asn Gly
                20                  25                  30

Phe Glu Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp
                35                  40                  45

Glu Lys Ile Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser
                50                  55                  60
```

362

Thr Tyr Leu Phe Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn
                65   70   75

Val Ser Ile Leu Ile Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr
                80   85   90

Lys Arg Pro Lys His Glu Asn His Lys His Ala Asp Val Ile Val
                95   100   105

Ala Pro Pro Thr Leu Pro Gly Arg Asp Glu Pro Tyr Thr Lys Gln
                110   115   120

Phe Thr Glu Cys Gly Glu Lys Gly Glu Tyr Ile His Phe Thr Pro
                125   130   135

Asp Leu Leu Leu Gly Lys Lys Gln Asn Glu Tyr Gly Pro Pro Gly
                140   145   150

Lys Leu Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe
                155   160   165

Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg Ala Lys Ser Lys
                170   175   180

Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser Gly Arg Asn
                185   190   195

Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg Ala Cys
                200   205   210

Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln Phe
                215   220   225

Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met
                230   235   240

Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His
                245   250   255

Asn Gln Glu Ala Pro Ser Leu Gln Asn Ile Lys Cys Asn Phe Arg
                260   265   270

Ser Thr Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr
                275   280   285

Ile Pro Met Val Thr Pro Pro Pro Pro Val Phe Ser Leu Leu
                290   295   300

Lys Ile Ser Gln Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly
                305   310   315

Ser Met Gly Gly Lys Asp Arg Leu Asn Arg Met Asn Gln Ala Ala
                320   325   330

Lys His Phe Leu Leu Gln Thr Val Glu Asn Gly Ser Trp Val Gly
                335   340   345

Met Val His Phe Asp Ser Thr Ala Thr Ile Val Asn Lys Leu Ile

363

Gln Ile Lys Ser Ser Asp Glu Arg Asn Thr Leu Met Ala Gly Leu
                365   370   375

Pro Thr Tyr Pro Leu Gly Gly Thr Ser Ile Cys Ser Gly Ile Lys
                380   385   390

Tyr Ala Phe Gln Val Ile Gly Glu Leu His Ser Gln Leu Asp Gly
                395   400   405

Ser Glu Val Leu Leu Leu Thr Asp Gly Glu Asp Asn Thr Ala Ser
                410   415   420

Ser Cys Ile Asp Glu Val Lys Gln Ser Gly Ala Ile Val His Phe
                425   430   435

Ile Ala Leu Gly Arg Ala Ala Asp Glu Ala Val Ile Glu Met Ser
                440   445   450

Lys Ile Thr Gly Gly Ser His Phe Tyr Val Ser Asp Glu Ala Gln
                455   460   465

Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Thr Ser Gly Asn
                470   475   480

Thr Asp Leu Ser Gln Lys Ser Leu Gln Leu Glu Ser Lys Gly Leu
                485   490   495

Thr Leu Asn Ser Asn Ala Trp Met Asn Asp Thr Val Ile Ile Asp
                500   505   510

Ser Thr Val Gly Lys Asp Thr Phe Phe Leu Ile Thr Trp Asn Ser
                515   520   525

Leu Pro Pro Ser Ile Ser Leu Trp Asp Pro Ser Gly Thr Ile Met
                530   535   540

Glu Asn Phe Thr Val Asp Ala Thr Ser Lys Met Ala Tyr Leu Ser
                545   550   555

Ile Pro Gly Thr Ala Lys Val Gly Thr Trp Ala Tyr Asn Leu Gln
                560   565   570

Ala Lys Ala Asn Pro Glu Thr Leu Thr Ile Thr Val Thr Ser Arg
                575   580   585

Ala Ala Asn Ser Ser Val Pro Pro Ile Thr Val Asn Ala Lys Met
                590   595   600

Asn Lys Asp Val Asn Ser Phe Pro Ser Pro Met Ile Val Tyr Ala
                605   610   615

Glu Ile Leu Gln Gly Tyr Val Pro Val Leu Gly Ala Asn Val Thr
                620   625   630

Ala Phe Ile Glu Ser Gln Asn Gly His Thr Glu Val Leu Glu Leu
                635   640   645

364

```
Leu Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys Asn Asp Gly Val
            650             655                     660

Tyr Ser Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly Arg Tyr Ser
            665             670                     675

Leu Lys Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg Leu Lys
            680             685                     690

Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp Val
            695             700                     705

Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp
            710             715                     720

Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser
            725             730                     735

Gly Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro
            740             745                     750

Asp Gln Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val
            755             760                     765

His Glu Asp Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn
            770             775                     780

Phe Asp Val Gly Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala
            785             790                     795

Ser Ile Leu Asp Leu Arg Asp Ser Phe Asp Asp Ala Leu Gln Val
            800             805                     810

Asn Thr Thr Asp Leu Ser Pro Lys Glu Ala Asn Ser Lys Glu Ser
            815             820                     825

Phe Ala Phe Lys Pro Glu Asn Ile Ser Glu Glu Asn Ala Thr His
            830             835                     840

Ile Phe Ile Ala Ile Lys Ser Ile Asp Lys Ser Asn Leu Thr Ser
            845             850                     855

Lys Val Ser Asn Ile Ala Gln Val Thr Leu Phe Ile Pro Gln Ala
            860             865                     870

Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr Pro Thr Pro Thr Pro
            875             880                     885

Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser Thr Leu
            890             895                     900

Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile Leu
            905             910                     915

Ser Thr Thr Ile

<210> 380
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<211> 3877
<212> DNA
<213> Homo sapiens

<400> 380
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gacccagagg agcaatgatg tagccacctc ctaaccttcc cttcttgaac 200

ccccagttat gccaggattt actagagagt gtcaactcaa ccagcaagcg 250

gctccttcgg cttaacttgt ggttggagga gagaaccttt gtggggctgc 300

gttctcttag cagtgctcag aagtgacttg cctgagggtg gaccagaaga 350

aaggaaaggt ccctcttgc tgttggctgc acatcaggaa ggctgtgatg 400

ggaatgaagg tgaaaacttg gagatttcac ttcagtcatt gcttctgcct 450

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ccaagaggca gaactcgttc tagaaggaaa tggatgcaag cagctccggg 550

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aaggaggagc tgcaggagag gagtgagcag ctcaggaatg ggcagtacca 950

agccagcgat gctgctggcc tgggtctgga caggagcccc ccagagaaaa 1000

cccaggccga cctcctggcc ttcctgcact cgcaggtgga caaggcagag 1050

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gccattgaat cagccttgga gaccctgaac aatcctgcag agaacagccc 1250

caatcaccgt ccttacacgg cctctgattt catagaaggg atctaccgaa 1300

cagaaaggga caaagggaca ttgtatgagc tcaccttcaa aggggaccac 1350

366

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taaaatggac cagaaaagaa aagaaaccat aaatatcgtg tcatattttc 2800
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367

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tttctgcttt acagaaaagg aaactcattc agactggtga tatcgtgatg 3250

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cttacctgtt taaataaacc aaagtatacc gtgtgaacca aacaatctct 3350

tttcaaaaca gggtgctcct cctggcttct ggcttccata agaagaaatg 3400

gagaaaaata tatatatata tatatatatt gtgaaagatc aatccatctg 3450

ccagaatcta gtgggatgga agttttttgct acatgttatc caccccaggc 3500

caggtggaag taactgaatt attttttaaa ttaagcagtt ctactcaatc 3550

accaagatgc ttctgaaaat tgcattttat taccatttca aactattttt 3600

taaaaataaa tacagttaac atagagtggt ttcttcattc atgtgaaaat 3650

tattagccag caccagatgc atgagctaat tatctctttg agtccttgct 3700

tctgtttgct cacagtaaac tcattgttta aaagcttcaa gaacattcaa 3750

gctgttggtg tgttaaaaaa tgcattgtat tgatttgtac tggtagttta 3800

tgaaatttaa ttaaaacaca ggccatgaat ggaaggtggt attgcacagc 3850

taataaaata tgatttgtgg atatgaa 3877
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<210> 381
<211> 532
<212> PRT
<213> Homo sapiens

<400> 381

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Met Met Met Val Arg Arg Gly Leu Leu Ala Trp Ile Ser Arg Val
 1               5                  10                  15

Val Val Leu Leu Val Leu Leu Cys Cys Ala Ile Ser Val Leu Tyr
                20                  25                  30

Met Leu Ala Cys Thr Pro Lys Gly Asp Glu Glu Gln Leu Ala Leu
                35                  40                  45
```

368

Pro Arg Ala Asn Ser Pro Thr Gly Lys Glu Gly Tyr Gln Ala Val
        50   55   60

Leu Gln Glu Trp Glu Glu Gln His Arg Asn Tyr Val Ser Ser Leu
        65   70   75

Lys Arg Gln Ile Ala Gln Leu Lys Glu Glu Leu Gln Glu Arg Ser
        80   85   90

Glu Gln Leu Arg Asn Gly Gln Tyr Gln Ala Ser Asp Ala Ala Gly
        95   100   105

Leu Gly Leu Asp Arg Ser Pro Pro Glu Lys Thr Gln Ala Asp Leu
        110   115   120

Leu Ala Phe Leu His Ser Gln Val Asp Lys Ala Glu Val Asn Ala
        125   130   135

Gly Val Lys Leu Ala Thr Glu Tyr Ala Ala Val Pro Phe Asp Ser
        140   145   150

Phe Thr Leu Gln Lys Val Tyr Gln Leu Glu Thr Gly Leu Thr Arg
        155   160   165

His Pro Glu Glu Lys Pro Val Arg Lys Asp Lys Arg Asp Glu Leu
        170   175   180

Val Glu Ala Ile Glu Ser Ala Leu Glu Thr Leu Asn Asn Pro Ala
        185   190   195

Glu Asn Ser Pro Asn His Arg Pro Tyr Thr Ala Ser Asp Phe Ile
        200   205   210

Glu Gly Ile Tyr Arg Thr Glu Arg Asp Lys Gly Thr Leu Tyr Glu
        215   220   225

Leu Thr Phe Lys Gly Asp His Lys His Glu Phe Lys Arg Leu Ile
        230   235   240

Leu Phe Arg Pro Phe Ser Pro Ile Met Lys Val Lys Asn Glu Lys
        245   250   255

Leu Asn Met Ala Asn Thr Leu Ile Asn Val Ile Val Pro Leu Ala
        260   265   270

Lys Arg Val Asp Lys Phe Arg Gln Phe Met Gln Asn Phe Arg Glu
        275   280   285

Met Cys Ile Glu Gln Asp Gly Arg Val His Leu Thr Val Val Tyr
        290   295   300

Phe Gly Lys Glu Glu Ile Asn Glu Val Lys Gly Ile Leu Glu Asn
        305   310   315

Thr Ser Lys Ala Ala Asn Phe Arg Asn Phe Thr Phe Ile Gln Leu
        320   325   330

Asn Gly Glu Phe Ser Arg Gly Lys Gly Leu Asp Val Gly Ala Arg

369

Phe Trp Lys Gly Ser Asn Val Leu Leu Phe Phe Cys Asp Val Asp
                    350   355   360

Ile Tyr Phe Thr Ser Glu Phe Leu Asn Thr Cys Arg Leu Asn Thr
                    365   370   375

Gln Pro Gly Lys Lys Val Phe Tyr Pro Val Leu Phe Ser Gln Tyr
                    380   385   390

Asn Pro Gly Ile Ile Tyr Gly His His Asp Ala Val Pro Pro Leu
                    395   400   405

Glu Gln Gln Leu Val Ile Lys Lys Glu Thr Gly Phe Trp Arg Asp
                    410   415   420

Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Ile Asn
                    425   430   435

Ile Gly Gly Phe Asp Leu Asp Ile Lys Gly Trp Gly Gly Glu Asp
                    440   445   450

Val His Leu Tyr Arg Lys Tyr Leu His Ser Asn Leu Ile Val Val
                    455   460   465

Arg Thr Pro Val Arg Gly Leu Phe His Leu Trp His Glu Lys Arg
                    470   475   480

Cys Met Asp Glu Leu Thr Pro Glu Gln Tyr Lys Met Cys Met Gln
                    485   490   495

Ser Lys Ala Met Asn Glu Ala Ser His Gly Gln Leu Gly Met Leu
                    500   505   510

Val Phe Arg His Glu Ile Glu Ala His Leu Arg Lys Gln Lys Gln
                    515   520   525

Lys Thr Ser Ser Lys Lys Thr
                    530

<210> 382
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
 ctcggggaaa gggacttgat gttgg 25

<210> 383
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383
 gcgaaggtga gcctctatct cgtgcc 26

<210> 384
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 384
 cagcctacac gtattgagg 19

<210> 385
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 385
 cagtcagtac aatcctggca taatatacgg ccaccatgat gcagtccc 48

<210> 386
<211> 1346
<212> DNA
<213> Homo sapiens

<400> 386
 gaaagaatgt tgtggctgct cttttttctg gtgactgcca ttcatgctga 50

 actctgtcaa ccaggtgcag aaaatgcttt taaagtgaga cttagtatca 100

 gaacagctct gggagataaa gcatatgcct gggataccaa tgaagaatac 150

 ctcttcaaag cgatggtagc tttctccatg agaaaagttc ccaacagaga 200

 agcaacagaa atttcccatg tcctactttg caatgtaacc cagagggtat 250

 cattctggtt tgtggttaca gacccttcaa aaaatcacac ccttcctgct 300

 gttgaggtgc aatcagccat aagaatgaac aagaaccgga tcaacaatgc 350

 cttctttcta aatgaccaaa ctctggaatt tttaaaaatc ccttccacac 400

 ttgcaccacc catggaccca tctgtgccca tctggattat tatatttggt 450

 gtgatatttt gcatcatcat agttgcaatt gcactactga ttttatcagg 500

 gatctggcaa cgtagaagaa agaacaaaga accatctgaa gtggatgacg 550

 ctgaagataa gtgtgaaaac atgatcacaa ttgaaaatgg catcccctct 600

 gatcccctgg acatgaaggg gggcatatta atgatgcctt catgacagag 650

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gatgagaggc tcacccctct ctgaagggct gttgttctgc ttcctcaaga 700

aattaaacat ttgtttctgt gtgactgctg agcatcctga aataccaaga 750

gcagatcata tattttgttt caccattctt cttttgtaat aaattttgaa 800

tgtgcttgaa agtgaaaagc aatcaattat acccaccaac accactgaaa 850

tcataagcta ttcacgactc aaaatattct aaaatatttt tctgacagta 900

tagtgtataa atgtggtcat gtggtatttg tagttattga tttaagcatt 950

tttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct 1000

aaggaaaaat aaattttcca gtggagaata catataatat ggtgtagaaa 1050

tcattgaaaa tggatccttt ttgacgatca cttatatcac tctgtatatg 1100

actaagtaaa caaaagtgag aagtaattat tgtaaatgga tggataaaaa 1150

tggaattact catatacagg gtggaatttt atcctgttat cacaccaaca 1200

gttgattata tattttctga atatcagccc ctaataggac aattctattt 1250

gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa 1300

agtaataatc atctcttttt aaaaaaaaaa aaaaaaaaaa aaaaaa 1346
```

<210> 387
<211> 212
<212> PRT
<213> Homo sapiens

<400> 387
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Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu
  1               5                  10                  15

    Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser
                  20                  25                  30

    Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn
                  35                  40                  45

    Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys
                  50                  55                  60

    Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys
                  65                  70                  75

    Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp Pro
                  80                  85                  90

    Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile
                  95                 100                 105

    Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
                 110                 115                 120
```

372

```
Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
             125                 130                 135

Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile
             140                 145                 150

Phe Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly
             155                 160                 165

Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp
             170                 175                 180

Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile Glu Asn Gly
             185                 190                 195

Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly Ile Leu Met Met
             200                 205                 210

Pro Ser
```

<210> 388
<211> 1371
<212> DNA
<213> Homo sapiens

<400> 388

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aactcaaact cctctctctg ggaaaacgcg gtgcttgctc ctcccggagt 50

ggccttggca gggtgttgga gccctcggtc tgccccgtcc ggtctctggg 100

gccaaggctg ggtttccctc atgtatggca agagctctac tcgtgcggtg 150

cttcttctcc ttggcataca gctcacagct ctttggccta tagcagctgt 200

ggaaatttat acctcccggg tgctggaggc tgttaatggg acagatgctc 250

ggttaaaatg cactttctcc agctttgccc ctgtgggtga tgctctaaca 300

gtgacctgga attttcgtcc tctagacggg ggacctgagc agtttgtatt 350

ctactaccac atagatccct tccaacccat gagtgggcgg tttaaggacc 400

gggtgtcttg ggatgggaat cctgagcggt acgatgcctc catccttctc 450

tggaaactgc agttcgacga caatgggaca tacacctgcc aggtgaagaa 500

cccacctgat gttgatgggg tgatagggga gatccggctc agcgtcgtgc 550

acactgtacg cttctctgag atccacttcc tggctctggc cattggctct 600

gcctgtgcac tgatgatcat aatagtaatt gtagtggtcc tcttccagca 650

ttaccggaaa aagcgatggg ccgaaagagc tcataaagtg gtggagataa 700

aatcaaaaga agaggaaagg ctcaaccaag agaaaaaggt ctctgtttat 750

ttagaagaca cagactaaca attttagatg gaagctgaga tgatttccaa 800
```

373

```
gaacaagaac cctagtattt cttgaagtta atggaaactt ttctttggct 850

tttccagttg tgacccgttt tccaaccagt tctgcagcat attagattct 900

agacaagcaa cacccctctg gagccagcac agtgctcctc catatcacca 950

gtcatacaca gcctcattat taaggtctta tttaatttca gagtgtaaat 1000

tttttcaagt gctcattagg ttttataaac aagaagctac attttttgccc 1050

ttaagacact acttacagtg ttatgacttg tatacacata tattggtatc 1100

aaaggggata aaagccaatt tgtctgttac atttcctttc acgtatttct 1150

tttagcagca cttctgctac taaagttaat gtgtttactc tctttccttc 1200

ccacattctc aattaaaagg tgagctaagc ctcctcggtg tttctgatta 1250

acagtaaatc ctaaattcaa actgttaaat gacatttta tttttatgtc 1300

tctccttaac tatgagacac atcttgtttt actgaatttc tttcaatatt 1350

ccaggtgata gatttttgtc g 1371
```

<210> 389
<211> 215
<212> PRT
<213> Homo sapiens

<400> 389

```
Met Tyr Gly Lys Ser Ser Thr Arg Ala Val Leu Leu Leu Leu Gly
 1               5                  10                  15

Ile Gln Leu Thr Ala Leu Trp Pro Ile Ala Ala Val Glu Ile Tyr
                20                  25                  30

Thr Ser Arg Val Leu Glu Ala Val Asn Gly Thr Asp Ala Arg Leu
                35                  40                  45

Lys Cys Thr Phe Ser Ser Phe Ala Pro Val Gly Asp Ala Leu Thr
                50                  55                  60

Val Thr Trp Asn Phe Arg Pro Leu Asp Gly Gly Pro Glu Gln Phe
                65                  70                  75

Val Phe Tyr Tyr His Ile Asp Pro Phe Gln Pro Met Ser Gly Arg
                80                  85                  90

Phe Lys Asp Arg Val Ser Trp Asp Gly Asn Pro Glu Arg Tyr Asp
                95                  100                 105

Ala Ser Ile Leu Leu Trp Lys Leu Gln Phe Asp Asp Asn Gly Thr
                110                 115                 120

Tyr Thr Cys Gln Val Lys Asn Pro Pro Asp Val Asp Gly Val Ile
                125                 130                 135

Gly Glu Ile Arg Leu Ser Val Val His Thr Val Arg Phe Ser Glu
```

374

```
                  140                  145                  150

     Ile His Phe Leu Ala Leu Ala Ile Gly Ser Ala Cys Ala Leu Met
                       155                  160                  165

     Ile Ile Ile Val Ile Val Val Val Leu Phe Gln His Tyr Arg Lys
                       170                  175                  180

     Lys Arg Trp Ala Glu Arg Ala His Lys Val Val Glu Ile Lys Ser
                       185                  190                  195

     Lys Glu Glu Glu Arg Leu Asn Gln Glu Lys Lys Val Ser Val Tyr
                       200                  205                  210

     Leu Glu Asp Thr Asp
                       215
```

<210> 390
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 390
 ccgaggccat ctagaggcca gagc 24

<210> 391
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 391
 acaggcagag ccaatggcca gagc 24

<210> 392
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392
 gagaggactg cgggagtttg ggacctttgt gcagacgtgc tcatg 45

<210> 393
<211> 471
<212> DNA
<213> Homo sapiens

<400> 393
 gcatttttgt ctgtgctccc tgatcttcag gtcaccacca tgaagttctt 50

agcagtcctg gtactcttgg gagtttccat ctttctggtc tctgcccaga 100

atccgacaac agctgctcca gctgacacgt atccagctac tggtcctgct 150

gatgatgaag cccctgatgc tgaaaccact gctgctgcaa ccactgcgac 200

cactgctgct cctaccactg caaccaccgc tgcttctacc actgctcgta 250

aagacattcc agttttaccc aaatgggttg gggatctccc gaatggtaga 300

gtgtgtccct gagatggaat cagcttgagt cttctgcaat tggtcacaac 350

tattcatgct cctgtgatt tcatccaact acttaccttg cctacgatat 400

cccctttatc tctaatcagt ttattttctt tcaaataaaa aataactatg 450

agcaacataa aaaaaaaaa a 471

<210> 394
<211> 90
<212> PRT
<213> Homo sapiens

<400> 394
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe
 1   5   10   15

Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr
                20   25   30

Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu
                35   40   45

Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr
                50   55   60

Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val
                65   70   75

Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
                80   85   90

<210> 395
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
gctccctgat cttcatgtca ccacc 25

<210> 396
<211> 26
<212> DNA
<213> Artificial Sequence

376

<220>
<223> Synthetic oligonucleotide probe

<400> 396
 cagggacaca ctctaccatt cgggag 26

<210> 397
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
 ccatctttct ggtctctgcc cagaatccga caacagctgc tc 42

<210> 398
<211> 907
<212> DNA
<213> Homo sapiens

<400> 398
 ggactctgaa ggtcccaagc agctgctgag gcccccaagg aagtggttcc 50

 aaccttggac ccctaggggt ctggatttgc tggttaacaa gataacctga 100

 gggcaggacc ccatagggga atgctacctc ctgcccttcc acctgccctg 150

 gtgttcacgg tggcctggtc cctccttgcc gagagagtgt cctgggtcag 200

 ggacgcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250

 ttggcaaggt ccagcgatgg tccggagtcc acacacagac tggcggcagg 300

 gcaggagggg gacagttctg ttgtgcttgg ttggacagta agagggtctt 350

 ggccagtcca gggtgggggg cggcaaactc cataaagaac cagagggtct 400

 gggcccggc cacagagtca tctgcccagc tcctctgctg ctggccagtg 450

 ggagtggcac gaggtggggc tttgtgccag taaaaccaca ggctggattt 500

 gcctgcgggc catggtccct gtctagggca gcaattctca accttcttgc 550

 tctcaggacc ccaaagagct ttcattgtat ctattgattt ttaccacatt 600

 agcaattaaa actgagaaat gggccgggca cggtggctca cgcctgtaat 650

 cccagcactt tgggaggccg aggcgggtgg atcacctgag atcaggagtt 700

 caagaccagc ctggccaaca tggtgaaacc ttgtctacta aaaatacaaa 750

 aaattagcca ggcacagtgg tgtgcactgg tagtcccagt tactcgggag 800

 gctgaggcag gaaaatcgct tgaacccagg aggcggacgt tgcggtgagc 850

 cgagatcgcg ccgctgattc cagcctgggc gacaagagtg agactccatc 900

377

tcacaca 907

<210> 399
<211> 120
<212> PRT
<213> Homo sapiens

<400> 399
Met Leu Pro Pro Ala Leu Pro Pro Ala Leu Val Phe Thr Val Ala
 1   5   10   15

Trp Ser Leu Leu Ala Glu Arg Val Ser Trp Val Arg Asp Ala Glu
                20   25   30

Asp Ala His Arg Leu Gln Pro Phe Val Thr Glu Arg Thr Leu Gly
                35   40   45

Lys Val Gln Arg Trp Ser Gly Val His Thr Gln Thr Gly Gly Arg
                50   55   60

Ala Gly Gly Gly Gln Phe Cys Cys Ala Trp Leu Asp Ser Lys Arg
                65   70   75

Val Leu Ala Ser Pro Gly Trp Gly Ala Ala Asn Ser Ile Lys Asn
                80   85   90

Gln Arg Val Trp Ala Pro Ala Thr Glu Ser Ser Ala Gln Leu Leu
                95   100   105

Cys Cys Trp Pro Val Gly Val Ala Arg Gly Gly Ala Leu Cys Gln
                110   115   120

<210> 400
<211> 893
<212> DNA
<213> Homo sapiens

<400> 400
gtcatgccag tgcctgctct gtgcctgctc tgggccctgg caatggtgac 50

ccggcctgcc tcagcggccc ccatgggcgg cccagaactg gcacagcatg 100

aggagctgac cctgctcttc catgggaccc tgcagctggg ccaggccctc 150

aacggtgtgt acaggaccac ggagggacgg ctgacaaagg ccaggaacag 200

cctgggtctc tatggccgca caatagaact cctggggcag gaggtcagcc 250

ggggccggga tgcagcccag gaacttcggg caagcctgtt ggagactcag 300

atggaggagg atattctgca gctgcaggca gaggccacag ctgaggtgct 350

gggggaggtg gcccaggcac agaaggtgct acgggacagc gtgcagcggc 400

tagaagtcca gctgaggagc gcctggctgg ccctgcctta ccgagaattt 450

gaggtcttaa aggctcacgc tgacaagcag agccacatcc tatgggccct 500

378

cacaggccac gtgcagcggc agaggcggga gatggtggca cagcagcatc 550

ggctgcgaca gatccaggag agactccaca cagcggcgct cccagcctga 600

atctgcctgg atggaactga ggaccaatca tgctgcaagg aacacttcca 650

cgccccgtga ggcccctgtg cagggaggag ctgcctgttc actgggatca 700

gccagggcgc cgggccccac ttctgagcac agagcagaga cagacgcagg 750

cggggacaaa ggcagaggat gtagccccat tggggagggg tggaggaagg 800

acatgtaccc tttcatgcct acacacccct cattaaagca gagtcgtggc 850

atttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 893

<210> 401
<211> 198
<212> PRT
<213> Homo sapiens

<400> 401
Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val
1   5   10   15

Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala
            20   25   30

Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu
            35   40   45

Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu
            50   55   60

Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
            65   70   75

Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu
            80   85   90

Leu Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu
            95   100   105

Gln Leu Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala
            110   115   120

Gln Ala Gln Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val
            125   130   135

Gln Leu Arg Ser Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu
            140   145   150

Val Leu Lys Ala His Ala Asp Lys Gln Ser His Ile Leu Trp Ala
            155   160   165

Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu Met Val Ala Gln
            170   175   180

379

Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His Thr Ala Ala
                185   190   195

Leu Pro Ala

<210> 402
<211> 1915
<212> DNA
<213> Homo sapiens

<400> 402
 ggcaacatgg ctcagcaggc ttgccccaga gccatggcaa agaatggact 50

 tgtaatttgc atcctggtga tcaccttact cctggaccag accaccagcc 100

 acacatccag attaaaagcc aggaagcaca gcaaacgtcg agtgagagac 150

 aaggatggag atctgaagac tcaaattgaa aagctctgga cagaagtcaa 200

 tgccttgaag gaaattcaag ccctgcagac agtctgtctc cgaggcacta 250

 aagttcacaa gaaatgctac cttgcttcag aaggtttgaa gcatttccat 300

 gaggccaatg aagactgcat ttccaaagga ggaatcctgg ttatccccag 350

 gaactccgac gaaatcaacg ccctccaaga ctatggtaaa aggagcctgc 400

 caggtgtcaa tgacttttgg ctgggcatca atgacatggt cacggaaggc 450

 aagtttgttg acgtcaacgg aatcgctatc tccttcctca actgggaccg 500

 tgcacagcct aacggtggca agcgagaaaa ctgtgtcctg ttctcccaat 550

 cagctcaggg caagtggagt gatgaggcct gtcgcagcag caagagatac 600

 atatgcgagt tcaccatccc taaataggtc tttctccaat gtgtcctcca 650

 agcaagattc atcataactt ataggttcat gatctctaag atcaagtaaa 700

 aatcataatt tttacttatt aaaaaattgc aacacaagat caatgtccat 750

 agcaatatga tagcatcagc caattttgct aacacatttc tttgggattt 800

 tgcccttcct ggggtatagg ggatcagaaa tattgatcca tgtgcacgca 850

 gataaaatgg cttctgctaa acagactaaa atctttctct ctagtctttc 900

 tcacttgtac aaacccagtt tgttttcaaa aaatcacagt agcaatgcaa 950

 ctcatcactc tagaaaagca agcttaggct acctgaaaga ttttcccttg 1000

 gaagtttagc gtatgtttga ctaacaaaaa ttccctacat cagagactct 1050

 aggtgctata taatccaaaa acttttcagc ctgttgctca ttctgtccca 1100

 tgctggcaat aataccttgt cagcccatta cccttatttt gaattgctcc 1150

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atctcctggt gggacttgta tcttgtctgc catatcagaa cacaaacccc 1200

tgaagaggtt ctgatttgat tttttttttt tcttcatgcc tacccttttt 1250

ttggaagttt ccagccgcaa tttgaaatga aatgacaagg tgtatatttg 1300

atcaattttc attcccacca ttgcattaca acctctaact taaatgggta 1350

accctaaggc atatcaaaga agcagattgc atgataaacg gaaatagaaa 1400

aaaagaacct acatttattt tgctttagca tccttactct cacctttat 1450

gagattgaga gtggacttac atttcctttt ttacattttc gtatatttat 1500

ttttttagc catcattata tgtttaagtc tattatgggc aaccaatctt 1550

tggaagctga aaactgaatt taaagaatgc tatcttggaa aattgcatac 1600

gtctgtgcaa ttttttattc tgcctagtgc tattctgctt gtttaactag 1650

attgtacaaa ataacttcat tgcttaatat caaattacaa agtttagact 1700

tggagggaaa tgggcttttt agaagcaaac aattttaaat atattttgtt 1750

cttcaaataa atagtgttta aacattgaat gtgttttgtg aacaatatcc 1800

cactttgcaa actttaacta cacatgcttg gaattaagtt ttagctgttt 1850

tcattgctca ataataaagc ctgaattctg atcaataaaa aaaaaaaaa 1900

aaaaaaaaaa aaaaa 1915

<210> 403
<211> 206
<212> PRT
<213> Homo sapiens

<400> 403
Met Ala Gln Gln Ala Cys Pro Arg Ala Met Ala Lys Asn Gly Leu
  1               5                  10                  15

Val Ile Cys Ile Leu Val Ile Thr Leu Leu Leu Asp Gln Thr Thr
                 20                  25                  30

Ser His Thr Ser Arg Leu Lys Ala Arg Lys His Ser Lys Arg Arg
                 35                  40                  45

Val Arg Asp Lys Asp Gly Asp Leu Lys Thr Gln Ile Glu Lys Leu
                 50                  55                  60

Trp Thr Glu Val Asn Ala Leu Lys Glu Ile Gln Ala Leu Gln Thr
                 65                  70                  75

Val Cys Leu Arg Gly Thr Lys Val His Lys Lys Cys Tyr Leu Ala
                 80                  85                  90

Ser Glu Gly Leu Lys His Phe His Glu Ala Asn Glu Asp Cys Ile
                 95                 100                 105
```

381

```
Ser Lys Gly Gly Ile Leu Val Ile Pro Arg Asn Ser Asp Glu Ile
                110                 115                 120

Asn Ala Leu Gln Asp Tyr Gly Lys Arg Ser Leu Pro Gly Val Asn
                125                 130                 135

Asp Phe Trp Leu Gly Ile Asn Asp Met Val Thr Glu Gly Lys Phe
                140                 145                 150

Val Asp Val Asn Gly Ile Ala Ile Ser Phe Leu Asn Trp Asp Arg
                155                 160                 165

Ala Gln Pro Asn Gly Gly Lys Arg Glu Asn Cys Val Leu Phe Ser
                170                 175                 180

Gln Ser Ala Gln Gly Lys Trp Ser Asp Glu Ala Cys Arg Ser Ser
                185                 190                 195

Lys Arg Tyr Ile Cys Glu Phe Thr Ile Pro Lys
                200                 205
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<210> 404
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
 cctggttatc cccaggaact ccgac 25

<210> 405
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 405
 ctcttgctgc tgcgacaggc ctc 23

<210> 406
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
 cgccctccaa gactatggta aaaggagcct gccaggtgtc aatgac 46

<210> 407
<211> 570
<212> DNA
<213> Homo sapiens

382

<400> 407
gcgaggaccg ggtataagaa gcctcgtggc cttgcccggg cagccgcagg 50

ttccccgcgc gccccgagcc cccgcgccat gaagctcgcc gccctcctgg 100

ggctctgcgt ggccctgtcc tgcagctccg ctgctgcttt cttagtgggc 150

tcggccaagc ctgtggccca gcctgtcgct gcgctggagt cggcggcgga 200

ggccggggcc gggaccctgg ccaaccccct cggcaccctc aacccgctga 250

agctcctgct gagcagcctg ggcatccccg tgaaccacct catagagggc 300

tcccagaagt gtgtggctga gctgggtccc caggccgtgg gggccgtgaa 350

ggccctgaag gccctgctgg gggccctgac agtgtttggc tgagccgaga 400

ctggagcatc tacacctgag gacaagacgc tgcccacccg cgagggctga 450

aaaccccgcc gcggggagga ccgtccatcc ccttcccccg gccctctca 500

ataaacgtgg ttaagagcaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 550

aaaaaaaaa aaaaaaaaa 570

<210> 408
<211> 104
<212> PRT
<213> Homo sapiens

<400> 408
Met Lys Leu Ala Ala Leu Leu Gly Leu Cys Val Ala Leu Ser Cys
1   5   10   15

Ser Ser Ala Ala Ala Phe Leu Val Gly Ser Ala Lys Pro Val Ala
                20   25   30

Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Gly
                35   40   45

Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu
                50   55   60

Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser
                65   70   75

Gln Lys Cys Val Ala Glu Leu Gly Pro Gln Ala Val Gly Ala Val
                80   85   90

Lys Ala Leu Lys Ala Leu Leu Gly Ala Leu Thr Val Phe Gly
                95   100

<210> 409
<211> 2089
<212> DNA
<213> Homo sapiens

<400> 409

383

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tgaaggactt ttccaggacc caaggccaca cactggaagt cttgcagctg 50

aagggaggca ctccttggcc tccgcagccg atcacatgaa ggtggtgcca 100

agtctcctgc tctccgtcct cctggcacag gtgtggctgg tacccggctt 150

ggcccccagt cctcagtcgc cagagacccc agcccctcag aaccagacca 200

gcagggtagt gcaggctccc agggaggaag aggaagatga gcaggaggcc 250

agcgaggaga aggccggtga ggaagagaaa gcctggctga tggccagcag 300

gcagcagctt gccaaggaga cttcaaactt cggattcagc ctgctgcgaa 350

agatctccat gaggcacgat ggcaacatgg tcttctctcc atttggcatg 400

tccttggcca tgacaggctt gatgctgggg gccacagggc cgactgaaac 450

ccagatcaag agagggctcc acttgcaggc cctgaagccc accaagcccg 500

ggctcctgcc ttccctcttt aagggactca gagagaccct ctcccgcaac 550

ctgaactgg gcctctcaca ggggagtttt gccttcatcc acaaggattt 600

tgatgtcaaa gagactttct tcaatttatc caagaggtat tttgatacag 650

agtgcgtgcc tatgaatttt cgcaatgcct cacaggccaa aaggctcatg 700

aatcattaca ttaacaaaga gactcggggg aaaattccca aactgtttga 750

tgagattaat cctgaaacca aattaattct tgtggattac atcttgttca 800

aagggaaatg gttgacccca tttgaccctg tcttcaccga agtcgacact 850

ttccacctgg acaagtacaa gaccattaag gtgcccatga tgtacggtgc 900

aggcaagttt gcctccacct ttgacaagaa ttttcgttgt catgtcctca 950

aactgcccta ccaaggaaat gccaccatgc tggtggtcct catggagaaa 1000

atgggtgacc acctcgccct tgaagactac ctgaccacag acttggtgga 1050

gacatggctc agaaacatga aaccagaaa catggaagtt ttctttccga 1100

agttcaagct agatcagaag tatgagatgc atgagctgct taggcagatg 1150

ggaatcagaa gaatcttctc acccttgct gaccttagtg aactctcagc 1200

tactggaaga aatctccaag tatccagggt tttacgaaga acagtgattg 1250

aagttgatga aaggggcact gaggcagtgg caggaatctt gtcagaaatt 1300

actgcttatt ccatgcctcc tgtcatcaaa gtggaccggc catttcattt 1350

catgatctat gaagaaacct ctggaatgct tctgtttctg ggcagggtgg 1400

tgaatccgac tctcctataa ttcaggacat gcataagcac ttcgtgctgt 1450
```

384

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agtagatgct gaatctgagg tatcaaacac acacaggata ccagcaatgg 1500

atggcagggg agagtgttcc ttttgttctt aactagttta gggtgttctc 1550

aaataaatac agtagtcccc acttatctga gggggataca ttcaaagacc 1600

cccagcagat gcctgaaacg gtggacagtg ctgaacctta tatatatttt 1650

ttcctacaca tacataccta tgataaagtt taatttataa attaggcaca 1700

gtaagagatt aacaataata acaacattaa gtaaaatgag ttacttgaac 1750

gcaagcactg caataccata acagtcaaac tgattataga gaaggctact 1800

aagtgactca tgggcgagga gcatagacag tgtggagaca ttgggcaagg 1850

ggagaattca catcctgggt gggacagagc aggacgatgc aagattccat 1900

cccactactc agaatggcat gctgcttaag acttttagat tgtttatttc 1950

tggaattttt catttaatgt ttttggacca tggttgacca tggttaactg 2000

agactgcaga aagcaaaacc atggataagg gaggactact acaaaagcat 2050

taaattgata catatttttt aaaaaaaaaa aaaaaaaaa 2089
```

<210> 410
<211> 444
<212> PRT
<213> Homo sapiens

<400> 410
```
Met Lys Val Val Pro Ser Leu Leu Leu Ser Val Leu Leu Ala Gln
 1               5                  10                  15

Val Trp Leu Val Pro Gly Leu Ala Pro Ser Pro Gln Ser Pro Glu
                20                  25                  30

Thr Pro Ala Pro Gln Asn Gln Thr Ser Arg Val Val Gln Ala Pro
                35                  40                  45

Arg Glu Glu Glu Glu Asp Glu Gln Glu Ala Ser Glu Glu Lys Ala
                50                  55                  60

Gly Glu Glu Glu Lys Ala Trp Leu Met Ala Ser Arg Gln Gln Leu
                65                  70                  75

Ala Lys Glu Thr Ser Asn Phe Gly Phe Ser Leu Leu Arg Lys Ile
                80                  85                  90

Ser Met Arg His Asp Gly Asn Met Val Phe Ser Pro Phe Gly Met
                95                  100                 105

Ser Leu Ala Met Thr Gly Leu Met Leu Gly Ala Thr Gly Pro Thr
                110                 115                 120

Glu Thr Gln Ile Lys Arg Gly Leu His Leu Gln Ala Leu Lys Pro
                125                 130                 135
```

385

Thr Lys Pro Gly Leu Leu Pro Ser Leu Phe Lys Gly Leu Arg Glu
                140   145   150

Thr Leu Ser Arg Asn Leu Glu Leu Gly Leu Ser Gln Gly Ser Phe
                155   160   165

Ala Phe Ile His Lys Asp Phe Asp Val Lys Glu Thr Phe Phe Asn
                170   175   180

Leu Ser Lys Arg Tyr Phe Asp Thr Glu Cys Val Pro Met Asn Phe
                185   190   195

Arg Asn Ala Ser Gln Ala Lys Arg Leu Met Asn His Tyr Ile Asn
                200   205   210

Lys Glu Thr Arg Gly Lys Ile Pro Lys Leu Phe Asp Glu Ile Asn
                215   220   225

Pro Glu Thr Lys Leu Ile Leu Val Asp Tyr Ile Leu Phe Lys Gly
                230   235   240

Lys Trp Leu Thr Pro Phe Asp Pro Val Phe Thr Glu Val Asp Thr
                245   250   255

Phe His Leu Asp Lys Tyr Lys Thr Ile Lys Val Pro Met Met Tyr
                260   265   270

Gly Ala Gly Lys Phe Ala Ser Thr Phe Asp Lys Asn Phe Arg Cys
                275   280   285

His Val Leu Lys Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val
                290   295   300

Val Leu Met Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr
                305   310   315

Leu Thr Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr
                320   325   330

Arg Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys
                335   340   345

Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg Ile
                350   355   360

Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg
                365   370   375

Asn Leu Gln Val Ser Arg Val Leu Arg Arg Thr Val Ile Glu Val
                380   385   390

Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile
                395   400   405

Thr Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe
                410   415   420

His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe Leu

386

425   430   435

Gly Arg Val Val Asn Pro Thr Leu Leu
                    440

<210> 411
<211> 636
<212> DNA
<213> Homo sapiens

<400> 411
 ctgggatcag ccactgcagc tccctgagca ctctctacag agacgcggac 50

 cccagacatg aggaggctcc tcctggtcac cagcctggtg gttgtgctgc 100

 tgtgggaggc aggtgcagtc ccagcaccca aggtccctat caagatgcaa 150

 gtcaaacact ggccctcaga gcaggaccca gagaaggcct ggggcgcccg 200

 tgtggtggag cctccggaga aggacgacca gctggtggtg ctgttccctg 250

 tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcagggc 300

 aggggcccca tccttccagg caccaaggcc tggatggaga ccgaggacac 350

 cctgggccgt gtcctgagtc ccgagcccga ccatgacagc ctgtaccacc 400

 ctccgcctga ggaggaccag ggcgaggaga ggccccggtt gtgggtgatg 450

 ccaaatcacc aggtgctcct gggaccggag gaagaccaag accacatcta 500

 ccacccccag tagggctcca ggggccatca ctgcccccgc cctgtcccaa 550

 ggcccaggct gttgggactg ggaccctccc taccctgccc cagctagaca 600

 aataaacccc agcaggcaaa aaaaaaaaaa aaaaa 636

<210> 412
<211> 151
<212> PRT
<213> Homo sapiens

<400> 412
 Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu
   1   5   10   15

 Trp Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met
                    20   25   30

 Gln Val Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp
                    35   40   45

 Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val
                    50   55   60

 Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu
                    65   70   75

Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys
              80   85   90

Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser Pro
              95   100   105

Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp
              110   115   120

Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln
              125   130   135

Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro
              140   145   150

Gln

<210> 413
<211> 1176
<212> DNA
<213> Homo sapiens

<400> 413
 agaaagctgc actctgttga gctccagggc gcagtggagg gagggagtga 50

 aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100

 caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150

 tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc 200

 gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250

 gtgcatttga tggcctgtat tttctccgca ctgagaatgg tgttatctac 300

 cagaccttct gtgacatgac ctctgggggt ggcggctgga ccctggtggc 350

 cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcgatcgct 400

 ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450

 tgggccaact acaacacctt tggatctgca gaggcggcca cgagcgatga 500

 ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550

 ggcacgtgcc aataagtcc cccatgcagc actggagaaa cagctccctg 600

 ctgaggtacc gcacggacac tggcttcctc cagacactgg gacataatct 650

 gtttggcatc taccagaaat atccagtgaa atatggagaa ggaaagtgtt 700

 ggactgacaa cggcccggtg atccctgtgg tctatgattt tggcgacgcc 750

 cagaaaacag catcttatta ctcaccctat ggccagcggg aattcactgc 800

 gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct 850

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tgtgtgctgg aatgagggtc accggatgta acactgagca tcactgcatt 900

ggtggaggag gatactttcc agaggccagt ccccagcagt gtggagattt 950

ttctggtttt gattggagtg gatatggaac tcatgttggt tacagcagca 1000

gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050

tgtgggaggg aacccagacc tctcctccca accatgagat cccaaggatg 1100

gagaacaact tacccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150

taaatcatat tgactcaaga aaaaaa 1176
```

<210> 414
<211> 313
<212> PRT
<213> Homo sapiens

<400> 414

```
Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg
 1               5                  10                  15

Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr
                20                  25                  30

Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys
                35                  40                  45

Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr
                50                  55                  60

Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly
                65                  70                  75

Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met
                80                  85                  90

Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly
                95                  100                 105

Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr
                110                 115                 120

Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys
                125                 130                 135

Asn Pro Gly Tyr Tyr Asp Ile Gln Ala Lys Asp Leu Gly Ile Trp
                140                 145                 150

His Val Pro Asn Lys Ser Pro Met Gln His Trp Arg Asn Ser Ser
                155                 160                 165

Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu Gln Thr Leu Gly
                170                 175                 180

His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val Lys Tyr Gly
                185                 190                 195
```

389

```
Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro Val Val
            200                 205                 210

Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser Pro
            215                 220                 225

Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val
            230                 235                 240

Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg
            245                 250                 255

Val Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Gly
            260                 265                 270

Tyr Phe Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly
            275                 280                 285

Phe Asp Trp Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser
            290                 295                 300

Arg Glu Ile Thr Glu Ala Ala Val Leu Leu Phe Tyr Arg
            305                 310
```

<210> 415
<211> 1281
<212> DNA
<213> Homo sapiens

<400> 415

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gcggagccgg cgccggctgc gcagaggagc cgctctcgcc gccgccacct 50

cggctgggag cccacgaggc tgccgcatcc tgccctcgga acaatgggac 100

tcggcgcgcg aggtgcttgg ccgcgctgc tcctggggac gctgcaggtg 150

ctagcgctgc tgggggccgc ccatgaaagc gcagccatgg cggcatctgc 200

aaacatagag aattctgggc ttccacacaa ctccagtgct aactcaacag 250

agactctcca acatgtgcct tctgaccata caaatgaaac ttccaacagt 300

actgtgaaac caccaacttc agttgcctca gactccagta atacaacggt 350

caccaccatg aaacctacag cggcatctaa tacaacaaca ccagggatgg 400

tctcaacaaa tatgacttct accaccttaa gtctacacc caaaacaaca 450

agtgtttcac agaacacatc tcagatatca acatccacaa tgaccgtaac 500

ccacaatagt tcagtgacat ctgctgcttc atcagtaaca atcacaacaa 550

ctatgcattc tgaagcaaag aaaggatcaa aatttgatac tgggagcttt 600

gttggtggta ttgtattaac gctgggagtt ttatctattc tttacattgg 650

atgcaaaatg tattactcaa gaagaggcat tcggtatcga accatagatg 700
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aacatgatgc catcatttaa ggaaatccat ggaccaagga tggaatacag 750

attgatgctg ccctatcaat taattttggt ttattaatag tttaaaacaa 800

tattctcttt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850

gtattacgta aatatgtaaa gattcttcaa ggtaacaagg gtttgggttt 900

tgaaataaac atctggatct tatagaccgt tcatacaatg gttttagcaa 950

gttcatagta agacaaacaa gtcctatctt ttttttttgg ctggggtggg 1000

ggcattggtc acatatgacc agtaattgaa agacgtcatc actgaaagac 1050

agaatgccat ctgggcatac aaataagaag tttgtcacag cactcaggat 1100

tttgggtatc ttttgtagct cacataaaga acttcagtgc ttttcagagc 1150

tggatatatc ttaattacta atgccacaca gaaattatac aatcaaacta 1200

gatctgaagc ataatttaag aaaaacatca acattttttg tgctttaaac 1250

tgtagtagtt ggtctagaaa caaaatactc c 1281

<210> 416
<211> 208
<212> PRT
<213> Homo sapiens

<400> 416
Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly
1   5   10   15

Thr Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala
                20   25   30

Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His
                35   40   45

Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser
                50   55   60

Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr
                65   70   75

Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met Lys
                80   85   90

Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr
                95   100   105

Asn Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser
                110   115   120

Val Ser Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val
                125   130   135

Thr His Asn Ser Ser Val Thr Ser Ala Ala Ser Ser Val Thr Ile

391

```
                140                  145                  150

Thr Thr Thr Met His Ser Glu Ala Lys Lys Gly Ser Lys Phe Asp
            155                  160                  165

Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr Leu Gly Val Leu
            170                  175                  180

Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser Arg Arg Gly
            185                  190                  195

Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile
            200                  205
```

<210> 417
<211> 1728
<212> DNA
<213> Homo sapiens

<400> 417

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cagccgggtc ccaagcctgt gcctgagcct gagcctgagc ctgagcccga 50

gccgggagcc ggtcgcgggg gctccgggct gtgggaccgc tgggccccca 100

gcgatggcga ccctgtgggg aggccttctt cggcttggct ccttgctcag 150

cctgtcgtgc ctggcgcttt ccgtgctgct gctggcgcag ctgtcagacg 200

ccgccaagaa tttcgaggat gtcagatgta aatgtatctg ccctccctat 250

aaagaaaatt ctgggcatat ttataataag aacatatctc agaaagattg 300

tgattgcctt catgttgtgg agcccatgcc tgtgcggggg cctgatgtag 350

aagcatactg tctacgctgt gaatgcaaat atgaagaaag aagctctgtc 400

acaatcaagg ttaccattat aatttatctc tccattttgg gccttctact 450

tctgtacatg gtatatctta ctctggttga gcccatactg aagaggcgcc 500

tctttggaca tgcacagttg atacagagtg atgatgatat tggggatcac 550

cagccttttg caaatgcaca cgatgtgcta gcccgctccc gcagtcgagc 600

caacgtgctg aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650

tccaagagca gcgaaagtct gtctttgacc ggcatgttgt cctcagctaa 700

ttgggaattg aattcaaggt gactagaaag aaacaggcag acaactggaa 750

agaactgact gggttttgct gggtttcatt ttaatacctt gttgatttca 800

ccaactgttg ctggaagatt caaaactgga agcaaaaact tgcttgattt 850

tttttcttg ttaacgtaat aatagagaca tttttaaaag cacacagctc 900

aaagtcagcc aataagtctt ttcctatttg tgacttttac taataaaaat 950
```

```
aaatctgcct gtaaattatc ttgaagtcct ttacctggaa caagcactct 1000

cttttttcacc acatagtttt aacttgactt tcaagataat tttcagggtt 1050

tttgttgttg ttgttttttg tttgtttgtt ttggtgggag aggggaggga 1100

tgcctgggaa gtggttaaca acttttttca agtcacttta ctaaacaaac 1150

ttttgtaaat agaccttacc ttctattttc gagtttcatt tatattttgc 1200

agtgtagcca gcctcatcaa agagctgact tactcatttg acttttgcac 1250

tgactgtatt atctgggtat ctgctgtgtc tgcacttcat ggtaaacggg 1300

atctaaaatg cctggtggct tttcacaaaa agcagatttt cttcatgtac 1350

tgtgatgtct gatgcaatgc atcctagaac aaactggcca tttgctagtt 1400

tactctaaag actaaacata gtcttggtgt gtgtggtctt actcatcttc 1450

tagtaccttt aaggacaaat cctaaggact tggacacttg caataaagaa 1500

attttatttt aaacccaagc ctccctggat tgataatata tacacatttg 1550

tcagcatttc cggtcgtggt gagaggcagc tgtttgagct ccaatatgtg 1600

cagctttgaa ctagggctgg ggttgtgggt gcctcttctg aaaggtctaa 1650

ccattattgg ataactggct tttttcttcc tatgtcctct ttggaatgta 1700

acaataaaaa taatttttga aacatcaa 1728
```

<210> 418
<211> 198
<212> PRT
<213> Homo sapiens

<400> 418

```
Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu
 1               5                  10                  15

Ser Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu
                20                  25                  30

Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile
                35                  40                  45

Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn
                50                  55                  60

Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu Pro Met
                65                  70                  75

Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu
                80                  85                  90

Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
                95                  100                 105
```

393

Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val
              110   115   120

Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly
              125   130   135

His Ala Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln
              140   145   150

Pro Phe Ala Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg
              155   160   165

Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys
              170   175   180

Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp Arg His Val
              185   190   195

Val Leu Ser

<210> 419
<211> 681
<212> DNA
<213> Homo sapiens

<400> 419
 gcacctgcga ccaccgtgag cagtcatggc gtactccaca gtgcagagag 50

 tcgctctggc ttctgggctt gtcctggctc tgtcgctgct gctgcccaag 100

 gccttcctgt cccgcgggaa gcggcaggag ccgccgccga cacctgaagg 150

 aaaattgggc cgatttccac ctatgatgca tcatcaccag gcaccctcag 200

 atggccagac tcctggggct cgtttccaga ggtctcacct gccgaggca 250

 tttgcaaagg ccaaaggatc aggtggaggt gctggaggag gaggtagtgg 300

 aagaggtctg atggggcaga ttattccaat ctacggtttt gggatttttt 350

 tatatatact gtacattcta tttaaggtaa gtagaatcat cctaatcata 400

 ttacatcaat gaaaatctaa tatggcgata aaaatcattg tctacattaa 450

 aacttcttat agttcataaa attatttcaa atccatcatc tctttaaatc 500

 ctgcctcctc ttcatgaggt acttaggata gccattattt cagtttcaca 550

 taagaatgtt tactcaatgt ttaagtgttt tgccccaaaa ttcacaacta 600

 acaaggcaga actaggactt gaacatggat cttttggttc ttaatccagt 650

 gagtgataca attcaatgca ctcccctgcc a 681

<210> 420
<211> 128
<212> PRT

394

<213> Homo sapiens

<400> 420
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Met Ala Tyr Ser Thr Val Gln Arg Val Ala Leu Ala Ser Gly Leu
  1           5                  10                  15

Val Leu Ala Leu Ser Leu Leu Leu Pro Lys Ala Phe Leu Ser Arg
             20                  25                  30

Gly Lys Arg Gln Glu Pro Pro Pro Thr Pro Glu Gly Lys Leu Gly
             35                  40                  45

Arg Phe Pro Pro Met Met His His His Gln Ala Pro Ser Asp Gly
             50                  55                  60

Gln Thr Pro Gly Ala Arg Phe Gln Arg Ser His Leu Ala Glu Ala
             65                  70                  75

Phe Ala Lys Ala Lys Gly Ser Gly Gly Gly Ala Gly Gly Gly Gly
             80                  85                  90

Ser Gly Arg Gly Leu Met Gly Gln Ile Ile Pro Ile Tyr Gly Phe
             95                 100                 105

Gly Ile Phe Leu Tyr Ile Leu Tyr Ile Leu Phe Lys Val Ser Arg
            110                 115                 120

Ile Ile Leu Ile Ile Leu His Gln
            125
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<210> 421
<211> 1630
<212> DNA
<213> Homo sapiens

<400> 421
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cggctcgagt gcagctgtgg ggagatttca gtgcattgcc tcccctgggt 50

gctcttcatc ttggatttga aagttgagag cagcatgttt tgcccactga 100

aactcatcct gctgccagtg ttactggatt attccttggg cctgaatgac 150

ttgaatgttt ccccgcctga gctaacagtc catgtgggtg attcagctct 200

gatgggatgt gttttccaga gcacagaaga caaatgtata ttcaagatag 250

actggactct gtcaccagga gagcacgcca aggacgaata tgtgctatac 300

tattactcca atctcagtgt gcctattggg cgcttccaga accgcgtaca 350

cttgatgggg gacatcttat gcaatgatgg ctctctcctg ctccaagatg 400

tgcaagaggc tgaccaggga acctatatct gtgaaatccg cctcaaaggg 450

gagagccagg tgttcaagaa ggcggtggta ctgcatgtgc ttccagagga 500

gcccaaagag ctcatggtcc atgtgggtgg attgattcag atgggatgtg 550
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395

ttttccagag cacagaagtg aaacacgtga ccaaggtaga atggatattt 600

tcaggacggc gcgcaaagga ggagattgta tttcgttact accacaaact 650

caggatgtct gtggagtact cccagagctg gggccacttc cagaatcgtg 700

tgaacctggt gggggacatt ttccgcaatg acggttccat catgcttcaa 750

ggagtgaggg agtcagatgg aggaaactac acctgcagta tccacctagg 800

gaacctggtg ttcaagaaaa ccattgtgct gcatgtcagc ccggaagagc 850

ctcgaacact ggtgaccccg gcagccctga ggcctctggt cttgggtggt 900

aatcagttgg tgatcattgt gggaattgtc tgtgccacaa tcctgctgct 950

ccctgttctg atattgatcg tgaagaagac ctgtggaaat aagagttcag 1000

tgaattctac agtcttggtg aagaacacga agaagactaa tccagagata 1050

aaagaaaaac cctgccattt tgaaagatgt gaaggggaga aacacattta 1100

ctccccaata attgtacggg aggtgatcga ggaagaagaa ccaagtgaaa 1150

aatcagaggc cacctacatg accatgcacc cagtttggcc ttctctgagg 1200

tcagatcgga caactcact tgaaaaaaag tcaggtgggg gaatgccaaa 1250

aacacagcaa gccttttgag aagaatggag agtcccttca tctcagcagc 1300

ggtggagact ctctcctgtg tgtgtcctgg ccactctac cagtgatttc 1350

agactcccgc tctcccagct gtcctcctgt ctcattgttt ggtcaataca 1400

ctgaagatgg agaatttgga gcctggcaga gagactggac agctctggag 1450

gaacaggcct gctgagggga ggggagcatg gacttggcct ctggagtggg 1500

acactggccc tgggaaccag gctgagctga gtggcctcaa acccccgtt 1550

ggatcagacc ctcctgtggg cagggttctt agtggatgag ttactgggaa 1600

gaatcagaga taaaaaccaa cccaaatcaa 1630

<210> 422
<211> 394
<212> PRT
<213> Homo sapiens

<400> 422
Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp
1   5   10   15

Tyr Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu
                20   25   30

Thr Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln
                35   40   45

396

Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser
                50   55   60

Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser
                65   70   75

Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu
                80   85   90

Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp
                95   100   105

Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg Leu
                110   115   120

Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
                125   130   135

Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu
                140   145   150

Ile Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val
                155   160   165

Thr Lys Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu
                170   175   180

Ile Val Phe Arg Tyr Tyr His Lys Leu Arg Met Ser Val Glu Tyr
                185   190   195

Ser Gln Ser Trp Gly His Phe Gln Asn Arg Val Asn Leu Val Gly
                200   205   210

Asp Ile Phe Arg Asn Asp Gly Ser Ile Met Leu Gln Gly Val Arg
                215   220   225

Glu Ser Asp Gly Gly Asn Tyr Thr Cys Ser Ile His Leu Gly Asn
                230   235   240

Leu Val Phe Lys Lys Thr Ile Val Leu His Val Ser Pro Glu Glu
                245   250   255

Pro Arg Thr Leu Val Thr Pro Ala Ala Leu Arg Pro Leu Val Leu
                260   265   270

Gly Gly Asn Gln Leu Val Ile Ile Val Gly Ile Val Cys Ala Thr
                275   280   285

Ile Leu Leu Leu Pro Val Leu Ile Leu Ile Val Lys Lys Thr Cys
                290   295   300

Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu Val Lys Asn Thr
                305   310   315

Lys Lys Thr Asn Pro Glu Ile Lys Glu Lys Pro Cys His Phe Glu
                320   325   330

Arg Cys Glu Gly Glu Lys His Ile Tyr Ser Pro Ile Ile Val Arg

397

Glu Val Ile Glu Glu Glu Glu Pro Ser Glu Lys Ser Glu Ala Thr
              350   355   360

Tyr Met Thr Met His Pro Val Trp Pro Ser Leu Arg Ser Asp Arg
              365   370   375

Asn Asn Ser Leu Glu Lys Lys Ser Gly Gly Gly Met Pro Lys Thr
              380   385   390

Gln Gln Ala Phe

<210> 423
<211> 963
<212> DNA
<213> Homo sapiens

<400> 423
ctatgaagaa gcttcctgga aaacaataag caaaggaaaa caaatgtgtc 50

ccatctcaca tggttctacc ctactaaaga caggaagatc ataaactgac 100

agatactgaa attgtaagag ttggaaacta cattttgcaa agtcattgaa 150

ctctgagctc agttgcagta ctcgggaagc catgcaggat gaagatggat 200

acatcacctt aaatattaaa actcggaaac cagctctcgt ctccgttggc 250

cctgcatcct cctcctggtg gcgtgtgatg ctttgattc tgctgatcct 300

gtgcgtgggg atggttgtcg ggctggtggc tctggggatt tggtctgtca 350

tgcagcgcaa ttacctacaa gatgagaatg aaaatcgcac aggaactctg 400

caacaattag caaagcgctt ctgtcaatat gtggtaaaac aatcagaact 450

aaagggcact ttcaaaggtc ataaatgcag cccctgtgac acaaactgga 500

gatattatgg agatagctgc tatgggttct caggcacaa cttaacatgg 550

gaagagagta agcagtactg cactgacatg aatgctactc tcctgaagat 600

tgacaaccgg aacattgtgg agtacatcaa agccaggact catttaattc 650

gttgggtcgg attatctcgc cagaagtcga atgaggtctg gaagtgggag 700

gatggctcgg ttatctcaga aaatatgttt gagtttttgg aagatggaaa 750

aggaaatatg aattgtgctt attttcataa tgggaaaatg caccctacct 800

tctgtgagaa caaacattat ttaatgtgtg agaggaaggc tggcatgacc 850

aaggtggacc aactacctta atgcaaagag gtggacagga taacacagat 900

aagggcttta ttgtacaata aaagatatgt atgaatgcat cagtagctga 950

398

aaaaaaaaaa aaa 963

<210> 424
<211> 229
<212> PRT
<213> Homo sapiens

<400> 424
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Met Gln Asp Glu Asp Gly Tyr Ile Thr Leu Asn Ile Lys Thr Arg
  1               5                  10                  15

Lys Pro Ala Leu Val Ser Val Gly Pro Ala Ser Ser Ser Trp Trp
             20                  25                  30

Arg Val Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val
             35                  40                  45

Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn
             50                  55                  60

Tyr Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln
             65                  70                  75

Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser Glu Leu
             80                  85                  90

Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr Asn
             95                  100                 105

Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn
             110                 115                 120

Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala
             125                 130                 135

Thr Leu Leu Lys Ile Asp Asn Arg Asn Ile Val Glu Tyr Ile Lys
             140                 145                 150

Ala Arg Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln Lys
             155                 160                 165

Ser Asn Glu Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu
             170                 175                 180

Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys
             185                 190                 195

Ala Tyr Phe His Asn Gly Lys Met His Pro Thr Phe Cys Glu Asn
             200                 205                 210

Lys His Tyr Leu Met Cys Glu Arg Lys Ala Gly Met Thr Lys Val
             215                 220                 225

Asp Gln Leu Pro
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<210> 425
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 425
tgcagcccct gtgacacaaa ctgg 24

<210> 426
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
ctgagataac cgagccatcc tcccac 26

<210> 427
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
gcttcctgac actaaggctg tctgctagtc agaattgcct caaaaagag 49

<210> 428
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 428
ccaccaatgg cagccccacc t 21

<210> 429
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 429
gactgccctc cctgcca 17

<210> 430
<211> 24
<212> DNA
<213> Artificial Sequence

400

<220>
<223> Synthetic oligonucleotide probe

<400> 430
 caaaaagcct ggaagtcttc aaag 24

<210> 431
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 431
 cagctggact gcaggtgcta 20

<210> 432
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 432
 cagtgagcac agcaagtgtc ct 22

<210> 433
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 433
 ggccacctcc ttgagtcttc agttccct 28

<210> 434
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 434
 caactactgg ctaaagctgg tgaa 24

<210> 435
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

401

<400> 435
 cctttctgta taggtgatac ccaatga 27

<210> 436
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 436
 tggccatccc taccagaggc aaaa 24

<210> 437
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 437
 ctgaagacga cgcggattac ta 22

<210> 438
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
 ggcagaaatg ggaggcaga 19

<210> 439
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
 tgctctgttg gctacggctt tagtccctag 30

<210> 440
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
 agcagcagcc atgtagaatg aa 22

<210> 441
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
 aatacgaaca gtgcacgctg at 22

<210> 442
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
 tccagagagc caagcacggc aga 23

<210> 443
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
 tctagccagc ttggctccaa ta 22

<210> 444
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
 cctggctcta gcaccaactc ata 23

<210> 445
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
 tcagtggccc taaggagatg ggcct 25

<210> 446
<211> 24
<212> DNA

403

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 446
 caggatacag tgggaatctt gaga 24

<210> 447
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 447
 cctgaagggc ttggagctta gt 22

<210> 448
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 448
 tctttggcca tttcccatgg ctca 24

<210> 449
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
 cccatggcga ggaggaat 18

<210> 450
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 450
 tgcgtacgtg tgccttcag 19

<210> 451
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 451
 cagcacccca ggcagtctgt gtgt 24

<210> 452
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 452
 aacgtgctac acgaccagtg tact 24

<210> 453
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
 cacagcatat tcagatgact aaatcca 27

<210> 454
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
 ttgtttagtt ctccaccgtg tctccacaga a 31

<210> 455
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
 tgtcagaatg caacctggct t 21

<210> 456
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 456

405

tgatgtgcct ggctcagaac 20

<210> 457
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 457
 tgcacctaga tgtccccagc accc 24

<210> 458
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 458
 aagatgcgcc aggcttctta 20

<210> 459
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 459
 ctcctgtacg gtctgctcac ttat 24

<210> 460
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 460
 tggctgtcag tccagtgtgc atgg 24

<210> 461
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
 gcatagggat agataagatc ctgctttat 29

<210> 462

406

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
 caaattaaag tacccatcag gagagaa 27

<210> 463
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 463
 aagttgctaa atatatacat tatctgcgcc aagtcca 37

<210> 464
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 464
 gtgctgccca caattcatga 20

<210> 465
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 465
 gtccttggta tgggtctgaa ttatat 26

<210> 466
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 466
 actctctgca ccccacagtc accactatct c 31

<210> 467
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 467
 ctgaggaacc agccatgtct ct 22

<210> 468
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 468
 gaccagatgc aggtacagga tga 23

<210> 469
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 469
 ctgccccttc agtgatgcca acctt 25

<210> 470
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 470
 gggtggaggc tcactgagta ga 22

<210> 471
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 471
 caatacaggt aatgaaactc tgcttctt 28

<210> 472
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

408

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<400> 472
 tcctcttaag cataggccat tttctcagtt tagaca 36

<210> 473
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
 ggtggtcttg cttggtctca c 21

<210> 474
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
 ccgtcgttca gcaacatgac 20

<210> 475
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
 accgcctacc gctgtgccca 20

<210> 476
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 476
 cagtaaaacc acaggctgga ttt 23

<210> 477
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 477
 cctgagagca agaaggttga gaat 24
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409

<210> 478
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
 tagacaggga ccatggcccg ca 22

<210> 479
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 479
 tgggctgtag aagagttgtt g 21

<210> 480
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 480
 tccacacttg gccagtttat 20

<210> 481
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 481
 cccaacttct ccctttgga ccct 24

<210> 482
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 482
 gtcccttcac tgtttagagc atga 24

<210> 483
<211> 26
<212> DNA

410

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 483
 actctccccc tcaacagcct cctgag 26

<210> 484
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 484
 gtggtcaggg cagatccttt 20

<210> 485
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
 acagatccag gagagactcc aca 23

<210> 486
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 486
 agcggcgctc ccagcctgaa t 21

<210> 487
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 487
 catgattggt cctcagttcc atc 23

<210> 488
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 488
atagagggct cccagaagtg 20

<210> 489
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 489
cagggccttc agggccttca c 21

<210> 490
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 490
gctcagccaa acactgtca 19

<210> 491
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 491
ggggccctga cagtgtt 17

<210> 492
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 492
ctgagccgag actggagcat ctacac 26

<210> 493
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 493

412

gtgggcagcg tcttgtc 17

<210> 494
<211> 1231
<212> DNA
<213> Homo Sapien

<400> 494
cccacgcgtc cgcgcagtcg cgcagttctg cctccgcctg ccagtctcgc 50

ccgcgatccc ggcccggggc tgtggcgtcg actccgaccc aggcagccag 100

cagcccgcgc gggagccgga ccgccgccgg aggagctcgg acggcatgct 150

gagccccctc ctttgctgaa gcccgagtgc ggagaagccc gggcaaacgc 200

aggctaagga gaccaaagcg gcgaagtcgc gagacagcgg acaagcagcg 250

gaggagaagg aggaggaggc gaacccagag aggggcagca aaagaagcgg 300

tggtggtggg cgtcgtggcc atggcggcgg ctatcgccag ctcgctcatc 350

cgtcagaaga ggcaagcccg cgagcgcgag aaatccaacg cctgcaagtg 400

tgtcagcagc cccagcaaag gcaagaccag ctgcgacaaa aacaagttaa 450

atgtcttttc ccgggtcaaa ctcttcggct ccaagaagag gcgcagaaga 500

agaccagagc ctcagcttaa gggtatagtt accaagctat acagccgaca 550

aggctaccac ttgcagctgc aggcggatgg aaccattgat ggcaccaaag 600

atgaggacag cacttacact ctgtttaacc tcatccctgt gggtctgcga 650

gtggtggcta tccaaggagt tcaaaccaag ctgtacttgg caatgaacag 700

tgagggatac ttgtacacct cggaactttt cacacctgag tgcaaattca 750

aagaatcagt gtttgaaaat tattatgtga catattcatc aatgatatac 800

cgtcagcagc agtcaggccg agggtggtat ctgggtctga caaagaagg 850

agagatcatg aaaggcaacc atgtgaagaa gaacaagcct gcagctcatt 900

ttctgcctaa accactgaaa gtggccatgt acaaggagcc atcactgcac 950

gatctcacgg agttctcccg atctggaagc gggaccccaa ccaagagcag 1000

aagtgtctct ggcgtgctga acggaggcaa atccatgagc cacaatgaat 1050

caacgtagcc agtgagggca aagaagggc tctgtaacag aaccttacct 1100

ccaggtgctg ttgaattctt ctagcagtcc ttcacccaaa agttcaaatt 1150

tgtcagtgac atttaccaaa caaacaggca gagttcacta ttctatctgc 1200

cattagacct tcttatcatc catactaaag c 1231

413

<210> 495
<211> 245
<212> PRT
<213> Homo Sapien

<400> 495
```
Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln
  1               5                  10                  15

Ala Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser
               20                  25                  30

Pro Ser Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val
               35                  40                  45

Phe Ser Arg Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg
               50                  55                  60

Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser
               65                  70                  75

Arg Gln Gly Tyr His Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp
               80                  85                  90

Gly Thr Lys Asp Glu Asp Ser Thr Tyr Thr Leu Phe Asn Leu Ile
               95                 100                 105

Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys
              110                 115                 120

Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu
              125                 130                 135

Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn
              140                 145                 150

Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser
              155                 160                 165

Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met
              170                 175                 180

Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu
              185                 190                 195

Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser Leu His
              200                 205                 210

Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr Lys
              215                 220                 225

Ser Arg Ser Val Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser
              230                 235                 240

His Asn Glu Ser Thr
              245
```

<210> 496

414

<211> 1471
<212> DNA
<213> Homo Sapien

<400> 496
ccaggatgga gctggggcct gtatagccat attattgttc tatgctacta 50

gacatggggg ggacttggtg aaaaaggtat tatccagcca gagggtctgg 100

gagccctgtc ttactgaacc tgggcaacct ggatattctg agacatattt 150

tggggggatt tcagtgaaaa aagtggggga tcccctccat ttagagtgta 200

gcaaaggaaa aaacaccaag gttgggttcc ttcctgacat tggcagtgcc 250

ccagtagggg tgggatgagc gaatattccc aaagctaaag tcccacaccc 300

tgtagattac aagagtggat ttggcaggag tgtgccccaa aatacagtgg 350

aaaggtgcct gaagatattt aaaccacgtc ttggaaattt agtgggtctt 400

ggctttggga taggtgaagt gaggacagac actggagagg agggaaaggg 450

gacgttttca ataggaggca aaactcgagg gtgggatcca ctgaggagta 500

cataggctgc tggatctggt ggagccagca ctgggcccac gggtggtaac 550

tggctgctgt ggaggggggt acgtgagggg ggggtctggg gcttatcctc 600

aggtcctgtg ggtggggcag cgagtcgggg cctgagcgtc aagagcatgc 650

cctagtgagc gggctcctct gggggagccc agcgcgctcc gggcgcctgc 700

cggtttgggg gtgtctcctc ccggggcgct atggcggcgc tggccagtag 750

cctgatccgg cagaagcggg aggtccgcga gcccgggggc agccggccgg 800

tgtcggcgca gcggcgcgtg tgtccccgcg gcaccaagtc cctttgccag 850

aagcagctcc tcatcctgct gtccaaggtg cgactgtgcg gggggcggcc 900

cgcgcggccg gaccgcggcc cggagcctca gctcaaaggc atcgtcacca 950

aactgttctg ccgccagggt ttctacctcc aggcgaatcc cgacggaagc 1000

atccagggca ccccagagga taccagctcc ttcacccact tcaacctgat 1050

ccctgtgggc ctccgtgtgg tcaccatcca gagcgccaag ctgggtcact 1100

acatggccat gaatgctgag ggactgctct acagttcgcc gcatttcaca 1150

gctgagtgtc gctttaagga gtgtgtcttt gagaattact acgtcctgta 1200

cgcctctgct ctctaccgcc agcgtcgttc tggccgggcc tggtacctcg 1250

gcctggacaa ggagggccag gtcatgaagg gaaaccgagt taagaagacc 1300

aaggcagctg cccactttct gcccaagctc ctggaggtgg ccatgtacca 1350

415

ggagccttct ctccacagtg tccccgaggc ctccccttcc agtccccctg 1400

cccctgaaa tgtagtccct ggactggagg ttccctgcac tcccagtgag 1450

ccagccacca ccacaacctg t 1471

<210> 497
<211> 225
<212> PRT
<213> Homo Sapien

<400> 497
Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val
 1   5   10   15

Arg Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val
                20   25   30

Cys Pro Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile
                35   40   45

Leu Leu Ser Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro
                50   55   60

Asp Arg Gly Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu
                65   70   75

Phe Cys Arg Gln Gly Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser
                80   85   90

Ile Gln Gly Thr Pro Glu Asp Thr Ser Ser Phe Thr His Phe Asn
                95   100   105

Leu Ile Pro Val Gly Leu Arg Val Val Thr Ile Gln Ser Ala Lys
                110   115   120

Leu Gly His Tyr Met Ala Met Asn Ala Glu Gly Leu Leu Tyr Ser
                125   130   135

Ser Pro His Phe Thr Ala Glu Cys Arg Phe Lys Glu Cys Val Phe
                140   145   150

Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala Leu Tyr Arg Gln Arg
                155   160   165

Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp Lys Glu Gly Gln
                170   175   180

Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala Ala Ala His
                185   190   195

Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu Pro Ser
                200   205   210

Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala Pro
                215   220   225

<210> 498

416

<211> 744
<212> DNA
<213> Homo Sapien

<400> 498
atggccgcgg ccatcgctag cggcttgatc cgccagaagc ggcaggcgcg 50

ggagcagcac tgggaccggc cgtctgccag caggaggcgg agcagcccca 100

gcaagaaccg cgggctctgc aacggcaacc tggtggatat cttctccaaa 150

gtgcgcatct cggcctcaa gaagcgcagg ttgcggcgcc aagatcccca 200

gctcaagggt atagtgacca ggttatattg caggcaaggc tactacttgc 250

aaatgcaccc cgatggagct ctcgatggaa ccaaggatga cagcactaat 300

tctacactct tcaacctcat accagtggga ctacgtgttg ttgccatcca 350

gggagtgaaa acagggttgt atatagccat gaatggagaa ggttacctct 400

acccatcaga acttttacc cctgaatgca gtttaaaga atctgttttt 450

gaaaattatt atgtaatcta ctcatccatg ttgtacagac aacaggaatc 500

tggtagagcc tggtttttgg gattaaataa ggaagggcaa gctatgaaag 550

ggaacagagt aaagaaaacc aaaccagcag ctcattttct acccaagcca 600

ttggaagttg ccatgtaccg agaaccatct ttgcatgatg ttggggaaac 650

ggtcccgaag cctggggtga cgccaagtaa aagcacaagt gcgtctgcaa 700

taatgaatgg aggcaaacca gtcaacaaga gtaagacaac atag 744

<210> 499
<211> 247
<212> PRT
<213> Homo Sapien

<400> 499
Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln
1   5   10   15

Ala Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Arg
                20   25   30

Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val
                35   40   45

Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg
                50   55   60

Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu
                65   70   75

Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala
                80   85   90

417

Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn
                95   100   105

Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys
                110   115   120

Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly Tyr Leu Tyr Pro
                125   130   135

Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe
                140   145   150

Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Leu Tyr Arg Gln Gln
                155   160   165

Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly Gln
                170   175   180

Ala Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ala Ala His
                185   190   195

Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser
                200   205   210

Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr Pro
                215   220   225

Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro
                230   235   240

Val Asn Lys Ser Lys Thr Thr
                245

<210> 500
<211> 2906
<212> DNA
<213> Homo Sapien

<400> 500
 ggggagagga attgaccatg taaaaggaga cttttttttt tggtggtggt 50

 ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100

 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150

 gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200

 acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250

 ttggtgtgtt ctgacataaa taataatct taaagcagct gttcccctcc 300

 ccacccccaa aaaaaggat gattggaaat gaagaaccga ggattcacaa 350

 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400

 gatattttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450

 ggtgtggtgg tgttttcctt tcttttgaa tttcccacaa gaggagagga 500

418

aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550

gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600

tttgtgccta tgttgactaa aattgacgga taattgcagt tggattttтc 650

ttcatcaacc tcctttтттt taaattttta ttcctттtgg tatcaagatc 700

atgcgtттtc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800

ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850

ataggtccta ggtttaacag ggccctattt gacccctgc ttgtggtgct 900

gctggctctt caacttcttg tggtggctgg tctggtgcgg gctcagacct 950

gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtgtt 1000

cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050

gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100

agcacttgag gcacttggaa atcctacagt tgagtaggaa ccatatcaga 1150

accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200

actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300

ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350

ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggtctgt 1400

ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450

aacctcacac cgctcataaa actagatgag ctggatctтt ctgggaatca 1500

tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550

aactgtggat gatacagtcc cagattcaag tgattgaacg gaatgccttt 1600

gacaaccttc agtcactagt ggagatcaac ctggcacaca ataatctaac 1650

attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700

atttacatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750

tggtggataa aagacatggc cccctcgaac acagcttgtt gtgcccggtg 1800

taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850

attacttcac atgctatgct ccggtgattg tggagccccc tgcagacctc 1900

aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950

419

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cctgacatct gtatcttgga ttactccaaa tggaacagtc atgacacatg 2000

gggcgtacaa agtgcggata gctgtgctca gtgatggtac gttaaatttc 2050

acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100

ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150

ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200

ccgtctcagg atgaggcacg gaccacagat aacaatgtgg tcccactcc 2250

agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300

gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350

agtgggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400

tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450

tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500

aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550

catggaaagc cacctgccca tgcctgctat cgagcatgag cacctaaatc 2600

actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650

ataaattcaa tacacagttc agtgcatgaa ccgttattga tccgaatgaa 2700

ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750

caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800

tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaacaa 2850

aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900

caaaaa 2906
```

<210> 501
<211> 640
<212> PRT
<213> Homo Sapien

<400> 501

```
Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly
1               5                   10                  15

Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu
                20                  25                  30

Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
                35                  40                  45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
                50                  55                  60
```

420

```
Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
                65              70              75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
                80              85              90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
                95             100             105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
               110             115             120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
               125             130             135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
               140             145             150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
               155             160             165

Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
               170             175             180

Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly
               185             190             195

Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
               200             205             210

Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
               215             220             225

Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
               230             235             240

Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
               245             250             255

Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
               260             265             270

Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
               275             280             285

Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His
               290             295             300

Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp
               305             310             315

Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys
               320             325             330

Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp
               335             340             345

Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro
```

421

```
                350                    355                    360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys
            365                    370                    375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn
            380                    385                    390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val
            395                    400                    405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp
            410                    415                    420
Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
            425                    430                    435
Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
            440                    445                    450
Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
            455                    460                    465
Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
            470                    475                    480
Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
            485                    490                    495
Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
            500                    505                    510
Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
            515                    520                    525
Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
            530                    535                    540
Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
            545                    550                    555
Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
            560                    565                    570
Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
            575                    580                    585
Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
            590                    595                    600
Tyr Lys Ser Pro Phe Asn His Thr Thr Val Asn Thr Ile Asn
            605                    610                    615
Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
            620                    625                    630
Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
            635                    640
```

422

<210> 502
<211> 2458
<212> DNA
<213> Homo Sapien

<400> 502
gcgccgggag cccatctgcc cccaggggca cggggcgcgg ggccggctcc 50

cgcccggcac atggctgcag ccacctcgcg cgcaccccga ggcgccgcgc 100

ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcggga tgtccctcct 200

ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaaa aagtggtgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag aacagaagg gccgagtggc ctttgcttcc 450

aatttcctgg caggagatgc ctccttgcag attgaacctc tgaagcccag 500

tgatgagggc cggtacacct gtaaggttaa gaattcaggg cgctacgtgt 550

ggagccatgt catcttaaaa gtcttagtga gaccatccaa gcccaagtgt 600

gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650

gtcatcctct ggcacagagc ccattgtgta ttactggcag cgaatccgag 700

agaaagaggg agaggatgaa cgtctgcctc ccaaatctag gattgactac 750

aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800

actgtaccag tgcacagcag gcaacgaagc tgggaaggaa agctgtgtgg 850

tgcgagtaac tgtacagtat gtacaaagca tcggcatggt tgcaggagca 900

gtgacaggca tagtggctgg agccctgctg atttttcctct tggtgtggct 950

gctaatccga aggaaagaca agaaagata tgaggaagaa gagagaccta 1000

atgaaattcg agaagatgct gaagctccaa aagcccgtct tgtgaaaccc 1050

agctcctctt cctcaggctc tcggagctca cgctctggtt cttcctccac 1100

tcgctccaca gcaaatagtg cctcacgcag ccagcggaca ctgtcaactg 1150

acgcagcacc ccagccaggg ctggccaccc aggcatacag cctagtgggg 1200

ccagaggtga gaggttctga accaaagaaa gtccaccatg ctaatctgac 1250

caaagcagaa accacaccca gcatgatccc cagccagagc agagccttcc 1300

423

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aaacggtctg aattacaatg gacttgactc ccacgctttc ctaggagtca 1350

gggtctttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400

ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450

agatgagcat tttccttata caataccaaa caagcaaaag gatgtaagct 1500

gattcatctg taaaaaggca tcttattgtg cctttagacc agagtaaggg 1550

aaagcaggag tccaaatcta tttgttgacc aggacctgtg gtgagaaggt 1600

tggggaaagg tgaggtgaat atacctaaaa cttttaatgt gggatatttt 1650

gtatcagtgc tttgattcac aattttcaag aggaaatggg atgctgtttg 1700

taaattttct atgcatttct gcaaacttat tggattatta gttattcaga 1750

cagtcaagca gaacccacag ccttattaca cctgtctaca ccatgtactg 1800

agctaaccac ttctaagaaa ctccaaaaaa ggaaacatgt gtcttctatt 1850

ctgacttaac ttcatttgtc ataaggtttg gatattaatt caagggggag 1900

ttgaaatagt gggagatgga gaagagtgaa tgagtttctc ccactctata 1950

ctaatctcac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000

aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050

ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150

agaaaataca acatgtcatt tatcaacgtc cttagaaaga attcttctag 2200

agaaaaaggg atctaggaat gctgaaagat tacccaacat accattatag 2250

tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300

tagaaaggga gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350

cgggcatggt gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400

gtgagccgag attatgccat tgcactccag cctgggtgac agagcgggac 2450

tccgtctc 2458
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<210> 503
<211> 373
<212> PRT
<213> Homo Sapien

<400> 503

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Met Ser Leu Leu Leu Leu Leu Leu Val Ser Tyr Tyr Val Gly
 1               5                  10                  15

Thr Leu Gly Thr His Thr Glu Ile Lys Arg Val Ala Glu Glu Lys
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424

                    20   25   30

Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp
                35   40   45

Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
                50   55   60

Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
                65   70   75

Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
                80   85   90

Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
                95   100   105

Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
                110   115   120

Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
                125   130   135

Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
                140   145   150

Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
                155   160   165

Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro
                170   175   180

Pro Lys Ser Arg Ile Asp Tyr Asn His Pro Gly Arg Val Leu Leu
                185   190   195

Gln Asn Leu Thr Met Ser Tyr Ser Gly Leu Tyr Gln Cys Thr Ala
                200   205   210

Gly Asn Glu Ala Gly Lys Glu Ser Cys Val Val Arg Val Thr Val
                215   220   225

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly
                230   235   240

Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu
                245   250   255

Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro
                260   265   270

Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val
                275   280   285

Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly
                290   295   300

Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln
                305   310   315

425

Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr
                320   325   330

Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro
                335   340   345

Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro
                350   355   360

Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val
                365   370

<210> 504
<211> 3060
<212> DNA
<213> Homo Sapien

<400> 504
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ccgccgccca cggcacggca gccaccatgg cgctcctgct gtgcttcgtg 100

ctcctgtgcg agtagtgga tttcgccaga agtttgagta tcactactcc 150

tgaagagatg attgaaaaag ccaaggggga aactgcctat ctgccatgca 200

aatttacgct tagtcccgaa gaccagggac cgctggacat cgagtggctg 250

atatcaccag ctgataatca gaaggtggat caagtgatta ttttatattc 300

tggagacaaa atttatgatg actactatcc agatctgaaa ggccgagtac 350

attttacgag taatgatctc aaatctggtg atgcatcaat aaatgtaacg 400

aatttacaac tgtcagatat tggcacatat cagtgcaaag tgaaaaaagc 450

tcctggtgtt gcaaataaga agattcatct ggtagttctt gttaagcctt 500

caggtgcgag atgttacgtt gatggatctg aagaaattgg aagtgacttt 550

aagataaaat gtgaaccaaa agaaggttca cttccattac agtatgagtg 600

gcaaaaattg tctgactcac agaaaatgcc cacttcatgg ttagcagaaa 650

tgacttcatc tgttatatct gtaaaaaatg cctcttctga gtactctggg 700

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gcgtctaaac gttgtccctc cttcaaataa agctggacta attgcaggag 800

ccattatagg aactttgctt gctctagcgc tcattggtct tatcatcttt 850

tgctgtcgta aaaagcgcag agaagaaaaa tatgaaaagg aagttcatca 900

cgatatcagg gaagatgtgc cacctccaaa gagccgtacg tccactgcca 950

gaagctacat cggcagtaat cattcatccc tggggtccat gtctccttcc 1000

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aacatggaag gatattccaa gactcagtat aaccaagtac caagtgaaga 1050

ctttgaacgc actcctcaga gtccgactct cccacctgct aagttcaagt 1100

acccttacaa gactgatgga attacagttg tataaatatg gactactgaa 1150

gaatctgaag tattgtatta tttgacttta ttttaggcct ctagtaaaga 1200

cttaaatgtt ttttaaaaaa agcacaaggc acagagatta gagcagctgt 1250

aagaacacat ctactttatg caatggcatt agacatgtaa gtcagatgtc 1300

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gtgacactga tagttaaaag atgttttatt atattttcaa taactaccac 1400

taacaaattt ttaacttttc atatgcatat tctgatatgt ggtcttttag 1450

gaaaagtatg gttaatagtt gatttttcaa aggaaatttt aaaattctta 1500

cgttctgttt aatgtttttg ctatttagtt aaatacattg aagggaaata 1550

cccgttcttt tccccttta tgcacacaac agaaacacgc gttgtcatgc 1600

ctcaaactat tttttatttg caactacatg atttcacaca attctcttaa 1650

acaacgacat aaaatagatt ccttgtata taaataactt acatacgctc 1700

cataaagtaa attctcaaag gtgctagaac aaatcgtcca cttctacagt 1750

gttctcgtat ccaacagagt tgatgcacaa tatataaata ctcaagtcca 1800

atattaaaaa cttaggcact tgactaactt taataaaatt ctcaaacta 1850

tatcaatatc taaagtgcat atattttta agaaagatta ttctcaataa 1900

cttctataaa aataagtttg atggtttggc ccatctaact tcactactat 1950

tagtaagaac ttttaacttt taatgtgtag taaggtttat ctacctttt 2000

tctcaacatg acaccaacac aatcaaaaac gaagttagtg aggtgctaac 2050

atgtgaggat taatccagtg attccggtca caatgcattc caggaggagg 2100

tacccatgtc actggaattg ggcgatatgg tttatttttt cttccctgat 2150

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cctcgataca ttcctggctt ttttctgggc aaagggtgcc acattggaag 2250

aggtggaaat ataagttctg aaatctgtag ggaagagaac acattaagtt 2300

aattcaaagg aaaaaatcat catctatgtt ccagatttct cattaaagac 2350

aaagttaccc acaacactga gatcacatct aagtgacact cctattgtca 2400

ggtctaaata cattaaaaac ctcatgtgta ataggcgtat aatgtataac 2450
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427

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aggtgaccaa tgttttctga atgcataaag aaatgaataa actcaaacac 2500

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ggaagcttgt aaggacatgc ttgttttagt ccagtggttt ccacagctgg 2600

ctaagccagg agtcacttgg aggcttttaa atacaaaaca ttggagctgg 2650

aggccattat ccttagcaaa ctaatgcaga aacagaaaat caactaccgc 2700

atgttctcac ttataagtgg gaggtaatga taagaactta tgaacacaaa 2750

gaaggaaaca atagacattg gagtctattt gagaggggag ggtgggagaa 2800

ggaaaaggag cagaaaagat aactattgag tactgccttc acacctgggt 2850

gatgaaataa tatgtacaac aaatccctgt gacacatgtt tacctatgga 2900

acaaaccttc atgtgtatcc ctaaacctaa aataaaagtt aaaaaaaaaa 2950

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aaaaaaaaaa 3060
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<210> 505
<211> 352
<212> PRT
<213> Homo Sapien

<400> 505
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Met Ala Leu Leu Leu Cys Phe Val Leu Leu Cys Gly Val Val Asp
 1               5                  10                  15

Phe Ala Arg Ser Leu Ser Ile Thr Thr Pro Glu Glu Met Ile Glu
             20                  25                  30

Lys Ala Lys Gly Glu Thr Ala Tyr Leu Pro Cys Lys Phe Thr Leu
             35                  40                  45

Ser Pro Glu Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Ile Ser
             50                  55                  60

Pro Ala Asp Asn Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser
             65                  70                  75

Gly Asp Lys Ile Tyr Asp Asp Tyr Tyr Pro Asp Leu Lys Gly Arg
             80                  85                  90

Val His Phe Thr Ser Asn Asp Leu Lys Ser Gly Asp Ala Ser Ile
             95                  100                 105

Asn Val Thr Asn Leu Gln Leu Ser Asp Ile Gly Thr Tyr Gln Cys
             110                 115                 120

Lys Val Lys Lys Ala Pro Gly Val Ala Asn Lys Lys Ile His Leu
             125                 130                 135
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428

Val Val Leu Val Lys Pro Ser Gly Ala Arg Cys Tyr Val Asp Gly
            140   145   150

Ser Glu Glu Ile Gly Ser Asp Phe Lys Ile Lys Cys Glu Pro Lys
            155   160   165

Glu Gly Ser Leu Pro Leu Gln Tyr Glu Trp Gln Lys Leu Ser Asp
            170   175   180

Ser Gln Lys Met Pro Thr Ser Trp Leu Ala Glu Met Thr Ser Ser
            185   190   195

Val Ile Ser Val Lys Asn Ala Ser Ser Glu Tyr Ser Gly Thr Tyr
            200   205   210

Ser Cys Thr Val Arg Asn Arg Val Gly Ser Asp Gln Cys Leu Leu
            215   220   225

Arg Leu Asn Val Val Pro Pro Ser Asn Lys Ala Gly Leu Ile Ala
            230   235   240

Gly Ala Ile Ile Gly Thr Leu Leu Ala Leu Ala Leu Ile Gly Leu
            245   250   255

Ile Ile Phe Cys Cys Arg Lys Lys Arg Arg Glu Glu Lys Tyr Glu
            260   265   270

Lys Glu Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys
            275   280   285

Ser Arg Thr Ser Thr Ala Arg Ser Tyr Ile Gly Ser Asn His Ser
            290   295   300

Ser Leu Gly Ser Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys
            305   310   315

Thr Gln Tyr Asn Gln Val Pro Ser Glu Asp Phe Glu Arg Thr Pro
            320   325   330

Gln Ser Pro Thr Leu Pro Pro Ala Lys Phe Lys Tyr Pro Tyr Lys
            335   340   345

Thr Asp Gly Ile Thr Val Val
            350

<210> 506
<211> 1705
<212> DNA
<213> Homo Sapien

<400> 506
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 ccagctgcct ccaggcagcc agccctcaag catcacttac aggaccagag 150

 ggacaagaca tgactgtgat gaggagctgc tttcgccaat ttaacaccaa 200

429

gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

agatgaattt caacagagg ctgcaaagcc tgtggacttt agccagaccc 300

ttctgccctc ctttgctggc gacagcctct caaatgcaga tggttgtgct 350

cccttgcctg ggttttaccc tgcttctctg gagccaggta tcaggggccc 400

agggccaaga attccacttt gggccctgcc aagtgaaggg ggttgttccc 450

cagaaactgt gggaagcctt ctgggctgtg aaagacacta tgcaagctca 500

ggataacatc acgagtgccc ggctgctgca gcaggaggtt ctgcagaacg 550

tctcggatgc tgagagctgt taccttgtcc acaccctgct ggagttctac 600

ttgaaaactg ttttcaaaaa ccaccacaat agaacagttg aagtcaggac 650

tctgaagtca ttctctactc tggccaacaa ctttgttctc atcgtgtcac 700

aactgcaacc cagtcaagaa aatgagatgt tttccatcag agacagtgca 750

cacaggcggt ttctgctatt ccggagagca ttcaaacagt tggacgtaga 800

agcagctctg accaaagccc ttggggaagt ggacattctt ctgacctgga 850

tgcagaaatt ctacaagctc tgaatgtcta gaccaggacc tccctccccc 900

tggcactggt ttgttccctg tgtcatttca aacagtctcc cttcctatgc 950

tgttcactgg acacttcacg cccttggcca tgggtcccat tcttggccca 1000

ggattattgt caaagaagtc attctttaag cagcgccagt gacagtcagg 1050

gaaggtgcct ctggatgctg tgaagagtct acagagaaga ttcttgtatt 1100

tattacaact ctatttaatt aatgtcagta tttcaactga agttctattt 1150

atttgtgaga ctgtaagtta catgaaggca gcagaatatt gtgccccatg 1200

cttctttacc cctcacaatc cttgccacag tgtggggcag tggatgggtg 1250

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atgaaaatca cactgtcttc tgatatctgc agggacagag cattggggtg 1400

ggggtaaggt gcatctgttt gaaaagtaaa cgataaaatg tggattaaag 1450

tgcccagcac aaagcagatc ctcaataaac atttcatttc ccacccacac 1500

tcgccagctc accccatcat cccttttccct tggtgccctc cttttttttt 1550

tatcctagtc attcttccct aatcttccac ttgagtgtca agctgacctt 1600

gctgatggtg acattgcacc tggatgtact atccaatctg tgatgacatt 1650

430

ccctgctaat aaaagacaac ataactccaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaa 1705

<210> 507
<211> 206
<212> PRT
<213> Homo Sapien

<400> 507
Met Asn Phe Gln Gln Arg Leu Gln Ser Leu Trp Thr Leu Ala Arg
 1   5   10   15

Pro Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met
                20   25   30

Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln
                35   40   45

Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln
                50   55   60

Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala
                65   70   75

Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg
                80   85   90

Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser
                95   100   105

Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val
                110   115   120

Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys
                125   130   135

Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln
                140   145   150

Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser
                155   160   165

Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu
                170   175   180

Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile
                185   190   195

Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
                200   205

<210> 508
<211> 924
<212> DNA
<213> Homo Sapien

<400> 508

431

aaggagcagc ccgcaagcac caagtgagag gcatgaagtt acagtgtgtt 50

tccctttggc tcctgggtac aatactgata ttgtgctcag tagacaacca 100

cggtctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150

gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaaat 200

gtcactatcc tgtccacatt ggagactctg cagatcatta gcccttaga 250

tgtgtgctgc gtgaccaaga acctcctggc gttctacgtg gacagggtgt 300

tcaaggatca tcaggagcca aaccccaaaa tcttgagaaa aatcagcagc 350

attgccaact ctttcctcta catgcagaaa actctgcggc aatgtcagga 400

acagaggcag tgtcactgca ggcaggaagc caccaatgcc accagagtca 450

tccatgacaa ctatgatcag ctggaggtcc acgctgctgc cattaaatcc 500

ctgggagagc tcgacgtctt tctagcctgg attaataaga atcatgaagt 550

aatgttctca gcttgatgac aaggaacctg tatagtgatc cagggatgaa 600

caccccctgt gcggtttact gtgggagaca gcccaccttg aaggggaagg 650

agatggggaa ggccccttgc agctgaaagt cccactggct ggcctcaggc 700

tgtcttattc cgcttgaaaa taggcaaaaa gtctactgtg gtatttgtaa 750

taaactctat ctgctgaaag ggcctgcagg ccatcctggg agtaaagggc 800

tgccttccca tctaatttat tgtaaagtca tatagtccat gtctgtgatg 850

tgagccaagt gatatcctgt agtacacatt gtactgagtg gtttttctga 900

ataaattcca tattttacct atga 924

<210> 509
<211> 177
<212> PRT
<213> Homo Sapien

<400> 509
Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu
 1   5   10   15

Ile Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile
                20   25   30

Ser Thr Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys
                35   40   45

Arg Ala Ile Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu
                50   55   60

Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys
                65   70   75

432

Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg Val Phe
                80   85   90

Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile Ser
                95   100   105

Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln
                110   115   120

Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn
                125   130   135

Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His
                140   145   150

Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu Ala
                155   160   165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala
                170   175

<210> 510
<211> 996
<212> DNA
<213> Homo Sapien

<400> 510
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 ccacctgtac acagccacag ccaggaacag ctaccacctg cagatccaca 400

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 tcctgtcccg gaggaacgag atcccccta ttcacttcaa cacccccata 750

 ccacggcggc acacccggag cgccgaggac gactcggagc gggacccccct 800

433

gaacgtgctg aagccccggg cccggatgac cccggccccg gcctcctgtt 850

cacaggagct cccgagcgcc gaggacaaca gcccgatggc cagtgaccca 900

ttaggggtgg tcaggggcgg tcgagtgaac acgcacgctg ggggaacggg 950

cccggaaggc tgccgcccct tcgccaagtt catctagggt cgctgg 996

<210> 511
<211> 251
<212> PRT
<213> Homo Sapien

<400> 511
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser
 1   5   10   15

Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
                20   25   30

Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala
                35   40   45

Thr Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His
                50   55   60

Val Asp Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile
                65   70   75

Arg Ser Glu Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser
                80   85   90

Arg Arg Tyr Leu Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser
                95   100   105

His Tyr Phe Asp Pro Glu Asn Cys Arg Phe Gln His Gln Thr Leu
                110   115   120

Glu Asn Gly Tyr Asp Val Tyr His Ser Pro Gln Tyr His Phe Leu
                125   130   135

Val Ser Leu Gly Arg Ala Lys Arg Ala Phe Leu Pro Gly Met Asn
                140   145   150

Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg Arg Asn Glu Ile Pro
                155   160   165

Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg His Thr Arg Ser
                170   175   180

Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val Leu Lys Pro
                185   190   195

Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln Glu Leu
                200   205   210

Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu Gly
                215   220   225

434

Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
                230   235   240

Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
                245   250

<210> 512
<211> 2015
<212> DNA
<213> Homo Sapien

<400> 512
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 ctagcaccgg gccacgccgc tctggaaact caaacgctga gcgctgagac 250

 ctcttctagg gcctcaaccc cagccggccc cattccagaa gcagagacca 300

 ggggagccaa gagaatttcc cctgcaagag agaccaggag tttcacaaaa 350

 acatctccca acttcatggt gctgatcgcc acctccgtgg agacatcagc 400

 cgccagtggc agccccgagg gagctggaat gaccacagtt cagaccatca 450

 caggcagtga tcccgaggaa gccatctttg acaccctttg caccgatgac 500

 agctctgaag aggcaaagac actcacaatg gacatattga cattggctca 550

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tctccataga ggctgggtca gcagtgggca aaacaacttc ctttgctggg 1250

agctctgctt cctcctacag cccctcggaa gccgccctca agaacttcac 1300

cccttcagag acaccgacca tggacatcgc aaccaagggg cccttcccca 1350

ccagcaggga ccctcttcct tctgtccctc cgactacaac caacagcagc 1400

cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450

gatgaagccc aacagccac gcccacgact gcccggacga ggccgaccac 1500

agacgtgagt gcaggtgaaa atggaggttt cctcctcctg cggctgagtg 1550

tggcttcccc ggaagacctc actgacccca gagtggcaga aaggctgatg 1600

cagcagctcc accgggaact ccacgcccac gcgcctcact tccaggtctc 1650

cttactgcgt gtcaggagag gctaacggac atcagctgca gccaggcatg 1700

tcccgtatgc caaaagaggg tgctgcccct agcctgggcc cccaccgaca 1750

gactgcagct gcgttactgt gctgagaggt acccagaagg ttcccatgaa 1800

gggcagcatg tccaagcccc taaccccaga tgtggcaaca ggaccctcgc 1850

tcacatccac cggagtgtat gtatggggag gggcttcacc tgttcccaga 1900

ggtgtccttg gactcacctt ggcacatgtt ctgtgtttca gtaaagagag 1950

acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttcactcagt 2000

gtggcccaaa aaaaa 2015

<210> 513
<211> 482
<212> PRT
<213> Homo Sapien

<400> 513
Met Gly Cys Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys
1   5   10   15

Trp Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg
                20   25   30

Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala
                35   40   45

Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu
                50   55   60

Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile
                65   70   75

Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg

436

```
Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu
                95                     100                     105

Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu
                110                    115                     120

Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro
                125                    130                     135

Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu
                140                    145                     150

Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr
                155                    160                     165

Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser
                170                    175                     180

Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser
                185                    190                     195

Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg
                200                    205                     210

Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile
                215                    220                     225

Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu
                230                    235                     240

Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile
                245                    250                     255

Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp
                260                    265                     270

Ile Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser
                275                    280                     285

Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile
                290                    295                     300

Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr
                305                    310                     315

Thr Glu Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro
                320                    325                     330

Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr
                335                    340                     345

Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu
                350                    355                     360

Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val
                365                    370                     375
```

437

Ser Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly
            380   385   390

Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro
            395   400   405

Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr
            410   415   420

Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro
            425   430   435

Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser Ser Arg Gly Thr
            440   445   450

Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr Met
            455   460   465

Lys Pro Gln Gln Pro Arg Pro Arg Leu Pro Gly Arg Gly Arg Pro
            470   475   480

Gln Thr

<210> 514
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 514
 gcggagcatc cgctgcggtc ctcgccgaga cccccgcgcg gattcgccgg 50

 tccttcccgc gggcgcgaca gagctgtcct cgcacctgga tggcagcagg 100

 ggcgccgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150

 cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200

 gaccaaaact aaactgaaat ttaaaatgtt cttcggggga aagggagct 250

 tgacttacac tttggtaata atttgcttcc tgacactaag gctgtctgct 300

 agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350

 gtcatctctt tctaagggaa tcagaggcaa tgagcccgta tatacttcaa 400

 ctcaagaaga ctgcattaat tcttgctgtt caacaaaaaa catatcaggg 450

 gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500

 acccaactgc tacctatttt tctgtcccaa cgaggaagcc tgtccattga 550

 aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600

 ttgaccagaa atttgccaag ccaagagtta ccccaggaag attctctctt 650

 acatggccaa ttttcacaag cagtcactcc cctagcccat catcacacag 700

438

attattcaaa gcccaccgat atctcatgga gagacacact ttctcagaag 750

tttggatcct cagatcacct ggagaaacta tttaagatgg atgaagcaag 800

tgcccagctc cttgcttata aggaaaaagg ccattctcag agttcacaat 850

tttcctctga tcaagaaata gctcatctgc tgcctgaaaa tgtgagtgcg 900

ctcccagcta cggtggcagt tgcttctcca cataccacct cggctactcc 950

aaagcccgcc acccttctac ccaccaatgc ttcagtgaca ccttctggga 1000

cttcccagcc acagctggcc accacagctc cacctgtaac cactgtcact 1050

tctcagcctc ccacgaccct catttctaca gtttttacac gggctgcggc 1100

tacactccaa gcaatggcta caacagcagt tctgactacc acctttcagg 1150

cacctacgga ctcgaaaggc agcttagaaa ccataccgtt tacagaaatc 1200

tccaacttaa ctttgaacac agggaatgtg tataacccta ctgcactttc 1250

tatgtcaaat gtggagtctt ccactatgaa taaaactgct tcctgggaag 1300

gtagggaggc cagtccaggc agttcctccc agggcagtgt tccagaaaat 1350

cagtacggcc ttccatttga aaaatggctt cttatcgggt ccctgctctt 1400

tggtgtcctg ttcctggtga taggcctcgt cctcctgggt agaatccttt 1450

cggaatcact ccgcaggaaa cgttactcaa gactggatta tttgatcaat 1500

gggatctatg tggacatcta aggatggaac tcggtgtctc ttaattcatt 1550

tagtaaccag aagcccaaat gcaatgagtt tctgctgact tgctagtctt 1600

agcaggaggt tgtattttga agacaggaaa atgccccctt ctgctttcct 1650

tttttttttt ggagacagag tcttgctctg ttgcccaggc tggagtgcag 1700

tagcacgatc tcggctctca ccgcaacctc cgtctcctgg gttcaagcga 1750

ttctcctgcc tcagcctcct aagtatctgg gattacaggc atgtgccacc 1800

acacctgggt gattttgta tttttagtag agacggggtt tcaccatgtt 1850

ggtcaggctg gtctcaaact cctgacctag tgatccaccc tcctcggcct 1900

cccaaagtgc tgggattaca ggcatgagcc accacagctg gcccccttct 1950

gttttatgtt tggtttttga gaaggaatga agtgggaacc aaattaggta 2000

attttgggta atctgtctct aaaatattag ctaaaaacaa agctctatgt 2050

aaagtaataa agtataattg ccatataaat ttcaaaattc aactggcttt 2100

tatgcaaaga aacaggttag gacatctagg ttccaattca ttcacattct 2150

439

tggttccaga taaaatcaac tgtttatatc aatttctaat ggatttgctt 2200

ttcttttttat atggattcct ttaaaactta ttccagatgt agttccttcc 2250

aattaaatat ttgaataaat cttttgttac tcaa 2284

<210> 515
<211> 431
<212> PRT
<213> Homo Sapien

<400> 515
Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile
 1   5   10   15

Ile Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu
                20   25   30

Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu
                35   40   45

Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln
                50   55   60

Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly
                65   70   75

Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala
                80   85   90

Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala
                95   100   105

Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile
                110   115   120

Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu
                125   130   135

Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val
                140   145   150

Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp
                155   160   165

Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp
                170   175   180

His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu
                185   190   195

Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
                200   205   210

Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
                215   220   225

Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala

440

Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
                245   250   255

Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro
                260   265   270

Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr
                275   280   285

Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr
                290   295   300

Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly
                305   310   315

Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu
                320   325   330

Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn
                335   340   345

Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Trp Glu Gly Arg
                350   355   360

Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly Ser Val Pro Glu Asn
                365   370   375

Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu Ile Gly Ser Leu
                380   385   390

Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly
                395   400   405

Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu
                410   415   420

Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
                425   430

<210> 516
<211> 2749
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 516
 ctcccacggt gtccagcgcc cagaatgcgg cttctggtcc tgctatgggg 50

 ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100

 gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

```
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400

caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaaccc agcccccagg 500

attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600

gaaaggactt ctcagtacac aggaacctct cctcacccag cgacctctcc 650

tcctgcaggg agctcccgcc cccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggcctgatcg ccttctgcag ccacctgctc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

ggacgtgatc tcgatgcctc ccctccacac atctgaggag gagctgggct 1000

tctcgaagtt tgtctcagcg tagggcagga ggccctcctg gccaggccag 1050

cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagctttc 1100

cacctcagcc tcagagtcca gctgcccgga ctccagggct ctccccaccc 1150

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catccctgat aggttcacat ccctgggcag agtaccaggc tgctgaccct 1300

cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350

aggaactcct gggcctcatg cccagtgtcg gaccctgcct tcctcccact 1400

ccagacccca ccttgtcttc cctccctggc gtcctcagac ttagtcccac 1450

ggtctcctgc atcagctggt gatgaagagg agcatgctgg ggtgagactg 1500

ggattctggc ttctctttga accacctgca tccagccctt caggaagcct 1550

gtgaaaaacg tgattcctgg ccccaccaag acccaccaaa accatctctg 1600
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442

ggcttggtgc aggactctga attctaacaa tgcccagtga ctgtcgcact 1650

tgagtttgag ggccagtggg cctgatgaac gctcacaccc cttcagctta 1700

gagtctgcat ttgggctgtg acgtctccac ctgccccaat agatctgctc 1750

tgtctgcgac accagatcca cgtggggact cccctgaggc ctgctaagtc 1800

caggccttgg tcaggtcagg tgcacattgc aggataagcc caggaccggc 1850

acagaagtgg ttgcctttnc catttgccct ccctggncca tgccttcttg 1900

cctttggaaa aaatgatgaa gaaaaccttg gctccttcct tgtctggaaa 1950

gggttacttg cctatgggtt ctggtggcta gagagaaaag tagaaaacca 2000

gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050

ctgaaggtga ctccgagtcc agcccctgg agaagggtc gggggtggtg 2100

gtaaagtagc acaactacta ttttttttct ttttccatta ttattgtttt 2150

ttaagacaga atctcgtgct gctgcccagg ctggagtgca gtggcacgat 2200

ctgcaaactc cgcctcctgg gttcaagtga ttcttctgcc tcagcctccc 2250

gagtagctgg gattacaggc acgcaccacc acctggct aattttttgta 2300

ctttttagtag agatggggtt tcaccatgtt ggccaggctg gtcttgaact 2350

cctgacctca aatgagcctc ctgcttcagt ctcccaaatt gccgggatta 2400

caggcatgag ccactgtgtc tggccctatt ccttttaaaa agtgaaatta 2450

agagttgttc agtatgcaaa acttggaaag atggaggaga aaaagaaaag 2500

gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550

tttgttgtac ttccttccac tcttttcttc ttcacataat ttgccggtgt 2600

tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650

tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700

gacctttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaa 2749

<210> 517
<211> 332
<212> PRT
<213> Homo Sapien

<400> 517
Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly
1   5   10   15

Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
            20   25   30

443

```
Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp
              35                  40                      45

His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg
              50                  55                      60

Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met
              65                  70                      75

Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu
              80                  85                      90

Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
              95                 100                     105

Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
             110                 115                     120

Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
             125                 130                     135

Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
             140                 145                     150

Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
             155                 160                     165

Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
             170                 175                     180

Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
             185                 190                     195

Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro
             200                 205                     210

Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala
             215                 220                     225

Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg
             230                 235                     240

Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu
             245                 250                     255

Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His
             260                 265                     270

Leu Leu Leu Trp Arg Lys Glu Ala Gln Ala Thr Glu Thr Gln
             275                 280                     285

Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys
             290                 295                     300

Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro
             305                 310                     315

Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val
```

444

Ser Ala

<210> 518
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 518
 ccctgcagtg cacctacagg gaag 24

<210> 519
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 519
 ctgtcttccc ctgcttggct gtgg 24

<210> 520
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 520
 ggtgcaggaa gggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 521
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 521
 ccagtgcaca gcaggcaacg aagc 24

<210> 522
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 522

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actaggctgt atgcctgggt gggc 24
```

<210> 523
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 523
```
gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43
```

<210> 524
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 524
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aatctcagca ccagccactc agagca 26
```

<210> 525
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 525
```
gttaaagagg gtgcccttcc agcga 25
```

<210> 526
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 526
```
tatcccaatg cctccccact gctc 24
```

<210> 527
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 527
```
gatgaacttg gcgaaggggc ggca 24
```

<210> 528

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 528
 agggaggatt atccttgacc tttgaagacc 30

<210> 529
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 529
 gaagcaagtg cccagctc 18

<210> 530
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 530
 cgggtccctg ctctttgg 18

<210> 531
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 531
 caccgtagct gggagcgcac tcac 24

<210> 532
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 532
 agtgtaagtc aagctccc 18

447